

XX Anderson CM, Davis RE, Clewenger W, Wiley SE, Miller SW, Szabo TR;
PI Ghosh SS;
XX WPI: 2000-365619/31.
DR N-PSDB: MADD00519.
XX
XX Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease -
XX
XX Claim 44; Page 172; 175pp; English.
XX
XX The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MTD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT1 from human brain.
XX
XX Sequence 297 AA:
S0
Query Match 100.0%; Score 1553; DB 21; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.2e-173;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGDHMSFLKDFLAGAANAASKTAVADIERVKLLQVHASKQISAEKQKGIIDCYVR 60
Db 1 MGDHMSFLKDFLAGAANAASKTAVADIERVKLLQVHASKQISAEKQKGIIDCYVR 60
QY 61 IPKEGFLSPWRGNLANVIRYFPTQALNFAFKDKYKQFLGVDNRHKOFRWYFAGNLASG 120
Db 61 IPKEGFLSPWRGNLANVIRYFPTQALNFAFKDKYKQFLGVDNRHKOFRWYFAGNLASG 120
QY 121 GAAGATSLCFYYPPLDFATRTLAADYGRRAOREFHGLGCIIRKFSDDLRLGYOGFNVSV 180
Db 121 GAAGATSLCFYYPPLDFATRTLAADYGRRAOREFHGLGCIIRKFSDDLRLGYOGFNVSV 180
QY 181 OGIIITRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLSYPTVRRRMQ 240
Db 181 OGIIITRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLSYPTVRRRMQ 240
QY 241 SGRKGADIMYGTVDCKWRIKADGAKAFKFGANSNVLRGNGAFVLYLDEIKRYV 297
Db 241 SGRKGADIMYGTVDCKWRIKADGAKAFKFGANSNVLRGNGAFVLYLDEIKRYV 297
RESULT 2
AAU01198
ID AAU01198 standard; Protein: 297 AA.
XX
XX AAU01198;
AC
XX
XX 07-SEP-2001 (first entry)
DE
XX Human adenine nucleotide translocator-1 (ANT-1) protein.
XX
XX Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
KW mitochondrial permeability transition pore component; cell survival;
KW mitochondrial core component; mitochondrial related disorder; cancer;
KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
XX

OS Homo sapiens.
XX
XX WO200132876-A2.
XX
XX 10-MAY-2001.
XX
XX 03-NOV-2000; 2000WO-US30535.
XX
XX 03-NOV-1999; 99US-0434354.
XX
XX (MITO-) MITOKOR.
XX
XX Murphy AN, Clewenger W, Wiley SE, Andreyev AV, Frigeri LG;
PI Velicelc G, Davis RE;
XX WPI: 2001-291054/30.
DR N-PSDB: MADS05901.
XX
XX New nucleic acid expression constructs, useful for screening for agents
PT that alter mitochondrial permeability transition (MPT), comprises
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
PT fused to energy transfer molecule -
XX
XX Disclosure: Fig 2; 186pp; English.
PS
XX
XX The present sequence represents human adenine nucleotide translocator-1
CC (ANT-1) protein. ANT proteins are mitochondrial permeability
CC transition (MPT) pore components responsible for mediating transport
CC of ADP across the mitochondrial inner membrane. ANT proteins interact
CC with other mitochondrial core components e.g. cyclophilins to
CC regulate MPT. The present invention relates to a novel nucleic acid
CC expression construct comprising a promoter operably linked to a
CC polynucleotide encoding a mitochondrial pore component polypeptide
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
CC expression construct can alter mitochondrial membrane permeability
CC transition and/or alter the interaction between mitochondrial core
CC components. The methods are useful for screening for agents that alter
CC MPT and/or cell survival. These agents are useful for the prevention or
CC treatment of diseases associated with altered mitochondrial function or
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC mitochondrial encephalopathy, lactic acidosis, stroke,
CC hyperproliferative disorders e.g. cancer, and deafness.
XX
XX Sequence 297 AA:

QY 1 MGDHMSFLKDFLAGAANAASKTAVADIERVKLLQVHASKQISAEKQKGIIDCYVR 60
Db 1 MGDHMSFLKDFLAGAANAASKTAVADIERVKLLQVHASKQISAEKQKGIIDCYVR 60
QY 61 IPKEGFLSPWRGNLANVIRYFPTQALNFAFKDKYKQFLGVDNRHKOFRWYFAGNLASG 120
Db 61 IPKEGFLSPWRGNLANVIRYFPTQALNFAFKDKYKQFLGVDNRHKOFRWYFAGNLASG 120
QY 121 GAAGATSLCFYYPPLDFATRTLAADYGRRAOREFHGLGCIIRKFSDDLRLGYOGFNVSV 180
Db 121 GAAGATSLCFYYPPLDFATRTLAADYGRRAOREFHGLGCIIRKFSDDLRLGYOGFNVSV 180
QY 181 OGIIITRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLSYPTVRRRMQ 240
Db 181 OGIIITRAAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLSYPTVRRRMQ 240
QY 241 SGRKGADIMYGTVDCKWRIKADGAKAFKFGANSNVLRGNGAFVLYLDEIKRYV 297
Db 241 SGRKGADIMYGTVDCKWRIKADGAKAFKFGANSNVLRGNGAFVLYLDEIKRYV 297
RESULT 3

ID	AAU10378	AAU10378 standard; Protein; 297 AA.
XX	AAU10378;	
XX	14-FEB-2002	(first entry)
XX	Human adenine nucleotide translocator 1 (ANT1).	
XX	Human; adenine nucleotide translocator; ANT;	
XX	mitochondrial matrix protein.	
XX	Homo sapiens.	
XX	MO200185944-A2.	
XX	15-NOV-2001.	
XX	11-MAY-2001; 2001WO-US15416.	
XX	11-MAY-2000; 2000US-0569327.	
XX	(MITO-) MITOKOR.	
XX	Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;	
XX	Ghosh SS, Moos WH, Pel Y, Carroll AK;	
XX	WPI: 2002-055598/07.	
XX	N-PSDB; AAS16688.	
XX	Novel recombinant expression construct for producing adenine nucleotide	
XX	translocator polypeptides, comprises a regulated promoter linked to	
XX	nucleic acid encoding the polypeptide	
XX	Claim 44; Fig 2; 147pp; English.	
XX	The invention relates to a recombinant expression construct (I)	
XX	comprising a regulated promoter operably linked to a nucleic acid	
XX	encoding an adenine nucleotide translocator (ANT) polypeptide. ANT	
XX	proteins mediate the exchange of ATP synthesised in the mitochondrial	
XX	matrix for ADP in the cytosol. (I) is useful for producing recombinant	
XX	ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and	
XX	culturing the host cell. (I) is also useful for targeting a polypeptide	
XX	of interest to a mitochondrial membrane, where ANT polypeptide is	
XX	expressed as a fusion protein with the polypeptide of interest.	
XX	Recombinant ANT polypeptide, or cells expressing the polypeptide, is	
XX	useful for identifying an agent that binds to an ANT polypeptide. ANT	
XX	ligand is useful for determining the presence of an ANT polypeptide,	
XX	preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating	
XX	ANT from a biological sample, where the ANT ligand is covalently or non-	
XX	covalently bound to a solid phase. Detectably labeled ANT ligand is also	
XX	useful for identifying an agent that interacts with an ANT polypeptide.	
XX	The present sequence represents the amino acid sequence of human ANT1.	
XX	Sequence 297 AA:	
XX	Query Match 100.0%; Score 1553; DB 23; Length 297;	
XX	Best Local Similarity 100.0%; Pred. No. 3.2e-173;	
XX	Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
XX	1 MGDHAWSLKDFLAGAVAAVAAVSKTAVAPIERVKLLQVHSHASKOISAEKQYKGIIDCVNR 60	
XX	1 MGDHAWSLKDFLAGAVAAVAAVSKTAVAPIERVKLLQVHSHASKOISAEKQYKGIIDCVNR 60	
XX	1 PKEGGFSLFEMNGNLAVNYRFFPTQALNFAFDKYLQFLGVGDNRKQFMRVAFAGNIASG 120	
XX	1 PKEGGFSLFEMNGNLAVNYRFFPTQALNFAFDKYLQFLGVGDNRKQFMRVAFAGNIASG 120	
XX	121 GAAGATSLCEVYPLDFAFARLADADVGRARQREFHGLDCCITIKFKSDGRLGLQGFNVSV 180	
XX	121 GAAGATSLCEVYPLDFAFARLADADVGRARQREFHGLDCCITIKFKSDGRLGLQGFNVSV 180	
XX	181 OGIIIRYRAAYEGVDTAKGLDPKKNVHIFVSMMIAQSVTAAGILSLYPEPTRRRMMQ 240	

[illegible]

QY 61 IPKEGFLSEWRGNLANVIRFPTQALNFAEKDKYKQLFLGVDNRHKOFRWRYFAGNLASG 120
 Db 61 IPKEGFLSEWRGNLANVIRFPTQALNFAEKDKYKQLFLGVDNRHKOFRWRYFAGNLASG 120
 QY 121 GAAGATSLCFYVPDLPARTRLAADYGR-AQREFHGLDCLIKFKPSGLNGLYOGFNVS 179
 Db 121 GAAGATSLCFYVPDLPARTRLAADYGR-AQREFHGLDCLIKFKPSGLNGLYOGFNVS 180
 QY 180 VGGIITVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIASVAVAGLSTYPTDVRRRMM 239
 Db 181 VGGIITVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIASVAVAGLSTYPTDVRRRMM 240
 QY 240 OSGRGADIMYTGTLDCMRKIAKDEGAKAFKFGANSNVLROMGAFVLYLDEIKKY 297
 Db 241 OSGRGADIMYTGTLDCMRKIAKDEGAKAFKFGANSNVLROMGAFVLYLDEIKKY 298

RESULT 5
 AA71032
 ID AA71032 standard; Protein: 298 AA.
 AC AA71032;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Human adenine nucleotide translocator ANT2.
 XX
 KW Human: adenine nucleotide translocator: ANT2; mitochondria; ADP: ATP;
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; neurotrophic;
 KW antiparkinsonian; cytoskeletal; antidiabetic; anticonvulsant; neuroleptic;
 KW antiportals; cerebroprotective; therapeutic; screening; psoriasis;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MDP;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.
 KM
 OS Homo sapiens.
 XX
 PN WO200026370-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 03-NOV-1999; 99WO-US25883.
 XX
 PR 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 XX
 DR WPI: 2000-365619/31.
 DR N-PSDB; AAD00520.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Claim 45; Page 172-173; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated

CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MDP), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT2 from human brain.
 XX
 SO Sequence 298 AA;
 Query Match 89.6%; Score 1391.5; DB 21; Length 298;
 Best Local Similarity 88.6%; Pred. No. 2,7e-154;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
 QY 1 MGDHMSFLKFLGAVAAVASKTAVAPIERVKLLQVHASKOISAERKGIIDCYVR 60
 Db 1 MTDALSFADKDFLAGVAAAIKSTVAIERVKLLQVHASKOITADKQKGIIDCYVR 60
 QY 61 IPKEGFLSEWRGNLANVIRFPTQALNFAEKDKYKQLFLGVDNRHKOFRWRYFAGNLASG 120
 Db 61 IPKEGFLSEWRGNLANVIRFPTQALNFAEKDKYKQLFLGVDNRHKOFRWRYFAGNLASG 120
 QY 121 GAAGATSLCFYVPDLPARTRLAADYGR-AQREFHGLDCLIKFKPSGLNGLYOGFNVS 179
 Db 121 GAAGATSLCFYVPDLPARTRLAADYGR-AQREFHGLDCLIKFKPSGLNGLYOGFNVS 180
 QY 180 VGGIITVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIASVAVAGLSTYPTDVRRRMM 239
 Db 181 VGGIITVRAAYFGVYDTAKGMLPDPKNVHIFVSWMIASVAVAGLSTYPTDVRRRMM 240
 QY 240 OSGRGADIMYTGTLDCMRKIAKDEGAKAFKFGANSNVLROMGAFVLYLDEIKKY 296
 Db 241 OSGRGADIMYTGTLDCMRKIAKDEGAKAFKFGANSNVLROMGAFVLYLDEIKKY 297

RESULT 6
 AA001199
 ID AA001199 standard; Protein: 298 AA.
 AC AA001199;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human adenine nucleotide translocator-2 (ANT-2) protein.
 XX
 KW Human: adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US30535.
 PF 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
 PI Velicelebi G, Davis RE;
 XX
 DR WPI: 2001-291054/30.
 DR N-PSDB; AAS05902.
 XX
 PT New nuclear acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX

PS Disclosure: Fig 2; 186pp; English.

XX
CC The present sequence represents human adenine nucleotide translocator-2
CC (ANT-2) protein. ANT proteins are mitochondrial permeability
CC transition (MPT) pore components responsible for mediating transport
CC of ADP across the mitochondrial inner membrane. ANT proteins interact
CC with other mitochondrial core components e.g. cyclophilins to
CC regulate MPT. The present invention relates to a novel nucleic acid
CC expression construct comprising a promoter operably linked to a
CC polynucleotide encoding a mitochondrial pore component polypeptide
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
CC expression construct can alter mitochondrial membrane permeability
CC transition and/or alter the interaction between mitochondrial core
CC components. The methods are useful for screening for agents that alter
CC MPT and/or cell survival. These agents are useful for the prevention or
CC treatment of diseases associated with altered mitochondrial function or
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC mitochondrial encephalopathy, lactic acidosis, stroke,
CC hyperproliferative disorders e.g. cancer, and deafness.

XX Sequence 298 AA;

Query Match 89.6%; Score 1391.5; DB 22; Length 298;
Best Local Similarity 88.6%; Pred. No. 2.7e-154;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHANSFLKDLFLAGAAVAAVSTAVAPIERVKLLLOVQHASKOISAEKQYKIIDCVVR 60
DB 1 MTDAAISFADKFLAGVAAVIASTAVAPIERVKLLLOVQHASKOITADKQYKIIDCVVR 60

QY 61 IPKEOGFLSWRGNLANVIRYPTQALNFAFKKQYKOLFLGVDKRRHOFRRYFAGNLASG 120
DB 61 IPKEOEVLSTWRGNLANVIRYPTQALNFAFKKQYKOLFLGVDKRRHOFRRYFAGNLASG 120

QY 121 GAAGATSLCFVYPLDFARTLADVGR- AOREFHGLGDCIIRIFKSDSRGLGYOGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTLADVGR- AOREFHGLGDCIIRIFKSDSRGLGYOGFNVS 180

QY 180 VGGIIRYRAVFGVYDTAKMLDPKKNVHIFVSMIAQSVTAAGLSYDFDVRRRMM 239
DB 181 VGGIIRYRAVFGIYDTAKMLDPKKNVHIFVSMIAQSVTAAGLSYDFDVRRRMM 240

QY 240 QSGRKGDIMYTGTLDCWKRIADDEGKAFKAGMSNVLRMGAGFVLVYDEIKKY 296
DB 241 QSGRKGDIMYTGTLDCWKRIADDEGKAFKAGMSNVLRMGAGFVLVYDEIKKY 297

RESULT 7

AAU10379

ID AAU10379 standard; Protein: 298 AA.

AC AAU10379;

DT 14-FEB-2002 (first entry)

DE Human adenine nucleotide translocator 2 (ANT2).

KW Human: adenine nucleotide translocator; ANT; ss;

KM mitochondrial matrix protein.

OS Homo sapiens.

PN WO200185944-A2.

PD 15-NOV-2001.

PF 11-MAY-2001; 2001WO-US15416.

PR 11-MAY-2000; 2000US-0569327.

PA (MITO-) MITOKOR.

XX
PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
PI Ghosh SS, Moos WH, Pei Y, Carroll AK;
XX
DR MPI: 2002-05598/07.
DR N-PSDB: AAS16689.

PT Novel recombinant expression construct for producing adenine nucleotide
PT translocator polypeptides, comprises a regulated promoter linked to
PT nucleic acid encoding the polypeptide

PS Claim 44: Fig 2; 147pp; English.

XX
CC The invention relates to a recombinant expression construct (I)
CC comprising a regulated promoter operably linked to a nucleic acid
CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC proteins mediate the exchange of ADP synthesised in the mitochondrial
CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
CC culturing the host cell. (I) is also useful for targeting a polypeptide
CC of interest to a mitochondrial membrane, where ANT polypeptide is
CC expressed as a fusion protein with the polypeptide of interest.
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC useful for identifying an agent that binds to an ANT polypeptide. ANT
CC ligand is useful for determining the presence of an ANT polypeptide,
CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
CC ANT from a biological sample, where the ANT ligand is covalently or non-
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC useful for identifying an agent that interacts with an ANT polypeptide.
XX The present sequence represents the amino acid sequence of human ANT2.

XX Sequence 298 AA;

Query Match 89.6%; Score 1391.5; DB 23; Length 298;
Best Local Similarity 88.6%; Pred. No. 2.7e-154;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHANSFLKDLFLAGAAVAAVSTAVAPIERVKLLLOVQHASKOISAEKQYKIIDCVVR 60
DB 1 MTDAAISFADKFLAGVAAVIASTAVAPIERVKLLLOVQHASKOITADKQYKIIDCVVR 60

QY 61 IPKEOGFLSWRGNLANVIRYPTQALNFAFKKQYKOLFLGVDKRRHOFRRYFAGNLASG 120
DB 61 IPKEOEVLSTWRGNLANVIRYPTQALNFAFKKQYKOLFLGVDKRRHOFRRYFAGNLASG 120

QY 121 GAAGATSLCFVYPLDFARTLADVGR- AOREFHGLGDCIIRIFKSDSRGLGYOGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTLADVGR- AOREFHGLGDCIIRIFKSDSRGLGYOGFNVS 180

QY 180 VGGIIRYRAVFGVYDTAKMLDPKKNVHIFVSMIAQSVTAAGLSYDFDVRRRMM 239
DB 181 VGGIIRYRAVFGIYDTAKMLDPKKNVHIFVSMIAQSVTAAGLSYDFDVRRRMM 240

QY 240 QSGRKGDIMYTGTLDCWKRIADDEGKAFKAGMSNVLRMGAGFVLVYDEIKKY 296
DB 241 QSGRKGDIMYTGTLDCWKRIADDEGKAFKAGMSNVLRMGAGFVLVYDEIKKY 297

RESULT 8

AAAY71033

ID AAAY71033 standard; Protein: 298 AA.

AC AAAY71033;

DT 29-AUG-2000 (first entry)

DE Human adenine nucleotide translocator ANT3.

KW Human: adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;

KM adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;

KW mitochondrial permeability transition; neuroprotective; neurotoxic;

KM antiParkinsonian; cytosolic; antiadrenergic; anticonvulsant; neuroleptic;

KM antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;

KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
KW mitochondrial diabetes and deafness; hyperproliferative disorder;
KW myoclonic epilepsy red ragged fibre syndrome.
XX
OS Homo sapiens.
XX
PN WO200026370-A2.
XX
PD 11-MAY-2000.
XX
PE 03-NOV-1999; 99WO-US25883.
XX
PR 03-NOV-1998; 98US-0185904.
XX 08-SEP-1999; 99US-0393441.
XX (MITO-) MITOKOR.
XX
PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI Ghosh SS;
XX
DR WPI: 2000-365619/31.
DR N-PSDB; AAD00521.
XX
PT Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease -
XX
PS Claim 46; Page 173-174; 175pp; English.
XX
XX The patent discloses a method to produce adenine nucleotide translocator
XX (ANT) proteins or ANT fusion proteins using recombinant expression
XX constructs. ANT is a nuclear encoded protein and a major component of
XX inner mitochondrial membrane. It mediates transport of adenosine
XX di/tri-phosphates across the mitochondrial inner membrane and also serves
XX as an important molecular component of the mitochondrial permeability
XX transition pore, a modulator of apoptosis. ANT is used to identify agents
XX or ligands that bind to, or interact with it. The ANT ligands are used to
XX detect or isolate ANT in a biological sample, and therapeutically for
XX regulating mitochondrial pore activity, for treating diseases associated
XX with altered mitochondrial function, including Alzheimer's, Parkinson's
XX and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
XX Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
XX encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
XX disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
XX epilepsy red ragged fibre syndrome. The present sequence is an
XX adenine nucleotide translocator ANT3 from human brain.
XX
SQ Sequence 298 AA;
Query Match 89.2%; Score 1385.5; DB 21; Length 298;
Best Local Similarity 87.2%; Pred. No. 1.4e-153;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

0Y 1 MGDHAWSLKDFLAGAANAASKTAVADIERVKLLQVHASKQISAKOKYKGIIDCYVR 60
Db 1 MTEQAIISPAKFLAGISAAISTKTAADIERVKLLQVHASKQIAADKOKYGIIDCYVR 60
0Y 61 IPKEGGVLSFWRGNLANVIRFPQALNPAFKDKYKQLFLGVNDHKKFWRFPANLNSG 120
Db 61 IPKEGGVLSFWRGNLANVIRFPQALNPAFKDKYKQLFLGVNDHKKFWRFPANLNSG 120
0Y 121 GAAGATSLCFVYPLDFAFTRLADYGR-AGREFHGLDCIIRKISGRLKLYGFPNVS 179
Db 121 GAAGATSLCFVYPLDFAFTRLADYGR-AGREFHGLDCIIRKISGRLKLYGFPNVS 179
0Y 180 VOGIITVRAAFGVYDTAKGMLDPKKNVHIEVSWMIAOSVYAVAGLSYPEDTVRRMM 239
Db 181 VOGIITVRAAFGVYDTAKGMLDPKKNVHIEVSWMIAOSVYAVAGLSYPEDTVRRMM 239
0Y 240 OSGRGADIMVTGYDCKRKIAKDGAKAFKSGAMSNVLRGKGAFVLYVDELKYY 297
Db 240 OSGRGADIMVTGYDCKRKIAKDGAKAFKSGAMSNVLRGKGAFVLYVDELKYY 297

Db 241 OSGRGADIMVTGYDCKRKIFRDEGKAFKSGAMSNVLRGKGAFVLYVDELKYY 298
RESULT 9
ID AAM39641
XX AAM39641 standard; Protein; 298 AA.
XX
AC AAM39641;
XX
DE 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2786.
XX
DE Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PE 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-052317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang Z, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou F, Goodrich R, Drmanac RT;
XX
DR WPI: 2001-442253/47.
DR N-PSDB; AAI58797.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
XX Example 4; SEQ ID NO 2786; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and
XX the encoded polypeptides (AAM38642-AAM42213) with nootropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemias and
XX C.N.S disorders.
XX Note: The sequence data for this patent did not form part of the printed
XX specification.
XX
SQ Sequence 298 AA;
Query Match 89.2%; Score 1385.5; DB 22; Length 298;
Best Local Similarity 87.2%; Pred. No. 1.4e-153;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

Qy	1	MGHAMSLKQPLAGAVAAASKTAAPVAIEEIVKLLQVQHASKQISAAKQYKGIIDCYR	60
		1 MTEQAIISFAKDFLWGGIAAIAIKSTRAVAPIEVEKLLQVQHASKQIAA03QYKGIIDCYR	60
Qy	61	IPKEGCEFSFPRGNLANIARYEPTQALNFAEKDKYKQLEFLGVDGRHKOEFMYEFGNLASG	120
		61 IPKEGCVLSFPRGNLANIARYEPTQALNFAEKDKYKQLEFLGVDGRHKOEFMYEFGNLASG	120
Qy	121	GAGATSLCEFYYPDLDFATRLADVGR - AQREFHGLDCDIKIFKSDJLGLGYOGFNVS	179
		121 GAGATSLCEFYYPDLDFATRLADVGR - AQREFHGLDCDIKIFKSDJLGLGYOGFNVS	179
Qy	180	VGGIITVAAEVGYDPAKGLPDKKNHIFVSMNIAQSVAAVGLLSYREDTVRRMM	239
		181 VGGIITVAAEVGYDPAKGLPDKKNHIFVSMNIAQSVAAVGLLSYREDTVRRMM	240
Qy	240	QSGRRGADIMVTGVVDCRRKIAKDEGAKAFKFGAMSNVLRMGAFVYLVEDEIKKYV	297
		241 QSGRRGADIMVTGVVDCRRKIFRDEGCKAFKFGAMSNVLRMGAFVYLVEDEIKKYV	298
RESULT	10		
AAU01200		AAU01200 standard; Protein: 298 AA.	
AAU01200:			
07-SEP-2001		(first entry)	
Human		adenine nucleotide translocator-3 (ANT-3) protein.	
Human:		adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin; mitochondrial core component; translocation pore component; cell survival; mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.	
Homo		sapiens.	
MO200132876-A2.			
10-MAY-2001.			
03-NOV-2000; 2000MO-US30535.			
03-NOV-1999; 99US-0434354.			
(MITO-) MITOKOR..			
Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Fritgeri LG; Vellicelebl G, Davis RE;			
WPI: 2001-291054/30.			
N-PSDB: AAS05903.			
New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule -			
Disclosure; Fig 2; 186pp; English.			
The present sequence represents human adenine nucleotide translocator-3 (ANT-3) protein. ANT proteins are mitochondrial permeability transition (MPT) pore components responsible for mediating transport of ADP across the mitochondrial inner membrane. ANT proteins interact with other mitochondrial core components e.g. cyclophilins to regulate MPT. The present invention relates to a novel nucleic acid expression construct comprising a promoter operably linked to a polynucleotide encoding a mitochondrial pore component polypeptide (e.g. ANT) fused to an energy transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel expression construct can alter mitochondrial membrane permeability			

[illegible]

CC The invention relates to a recombinant expression construct (1)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (1) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (1) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT3.
 CC
 CC
 CC Sequence 298 AA:
 CC
 CC

SQ Sequence 298 AA;

Query Match	89.2%	Score 1385.5;	DB 23;	Length 299;
Best Local Similarity	87.2%;	Pred. No. 1.4e-153;		
Matches 260; Conservative	21;	Mismatches 16;	Indels 1;	Gaps 1;

QY	1	MGSHAFSLKDFELACGAAVAAVSKTVAATIEVKKLLLOVHASQOISERKQKIIDCVR	60
Db	1	MTQOALSPAKDFLAGIQAALISKTAVIDIEVKLLLOVHASQIQAADQYKSIYDVCIR	60
QY	61	IRPEQGFSLFMWGNLANVITRFPFOALNEAKDKYKOLFLGAGYDRKHQKTRPFAAGLASG	12
Db	61	IRPEQGVLSFMWGNLANVITRFPFOALNEAKDKYKOLFLGAGYDKHQKTRFPFAAGLASG	12
QY	121	GAGATSLCFEYVPLDFARTRLAADVGR - AGRPEFGGDCDCTIKTFKPSDGLRGLYOGEFNS	17
Db	121	GAGATSLCFEYVPLDFARTRLAADVGKSGTTRERRGGLDCLVITITSDGIRGLYOGEFNS	18
QY	180	VGGIIITYRAATGCVYDTAKGMLPDKKNVHIFVSMIAQSVATAVAGLSTPFDTVRRMM	23
Db	181	VGGIIITYRAATGCVYDTAGKMLPDKKNVHIVSMIAQSVATAVAGVSTPFDTVRRMM	24
QY	240	QSGRKADIMTYGVDCMKTLAKDGAATFAFGKAMSVNLGKMGATVLYUDEIKKYV	297
Db	241	QSGRKADIMTYGVDCMKTLRDDGGAATFAFGKAMSVNLGKMGATVLYUDEIKKYV	298

RESULT	12
AAM41427	
ID	AAM41427 standard; Protein; 323 AA.

AC	AA041427;	
XX		
DT	22-OCT-2001	(first entry)
XX		
DE	Human polypeptide SEQ ID NO 6358.	
XX		
XX	Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;	
KW	peripheral nervous system; neuropathy; central nervous system; CNS;	
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;	
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;	
KW	chemokine; thrombolytic; drug screening; arthritis; inflammation;	
XX	leukaemia.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200153312-A1.	
XX		
PD	26-JUL-2001.	
XX		
PF	26-DEC-2000; 2000MO-US34263.	
XX		
PR	21-JAN-2000; 2000US-0486725.	
PR	25-APR-2000; 2000US-0552317.	
PR	09-JUL-2000; 2000US-0598042.	

PR 19-JUL-2000; 2000US-0620312
PR 03-AUG-2000; 2000US-0653450
PR 14-SEP-2000; 2000US-0662191
PR 19-OCT-2000; 2000US-0693036
PR 29-NOV-2000; 2000US-0727344

(HYSE-) HYSEQ INC

Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D, Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA, Zhou P, Goodrich R, Drmanac RT;

WPI; 2001-442253/47.
N-PSDB; AAI60583.

Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -

Example 2; SEQ ID NO 6358; 10078bp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AA038642-AA042213) with neurotrophic
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

specification.

SQ Sequence 323 AA.

Query Match	89.2%;	Score 1385.5;	DB 22;	Length 323;
Best Local Similarity	87.2%;	Pred. No. 1.6e-153;		
Matches 260;	Conservative 21;	Mismatches 16;	Indels 1;	Gaps 1.

Oy	1	MGAAMSLKQPLFAGAAAAASKTAAVPIEBVKLLLOVOHSAKSIOSEKQYGIIDCVR	60
Db	26	MTEDAIISAFKDELGGTAIAASTKAAPAEIKVKLLLOVOHASKOIADAKOYKGIIVDCIR	85
Oy	61	IPKEOGELSFWRGMLANVIYRIPTQALNEAFKKDYKOLELFGVDHRHQEFREYAGNLASG	120
Db	86	IPKEOGVLSPWGRMLANVIYREFPTQALNFAFKDKYKQIFLGVDKHQOFWRYPAGNLASG	145
Oy	121	GAAATLSLCFFYPIIDFARTRLAADVGRR-AOREFHGIGDCLIIKIEKSDGLRGLYOGFNVS	179
Db	146	GAAATSLSCFFYPIIDFARTRLAADVGSGTEREERERGIGDCLIVKTKITSDDGIRGLYOQSYS	205
Oy	180	VQGIIIRAAAFEGYVDIAKGMLEDPDKVVNHIFVSMIMIASQSTYAAGLGLSYPDFDIARRMMX	239
Db	206	VQGIIRRAAFLGYVDIAKGMLEDPKKNTHILYVSMIMIQYTAAVAGVSYSPFDIVRRMMX	265
Oy	240	OSGRKGADIMTGVIDCMRKITAKDEGAKAPFKGMSVNLRGMGAPLVLIYDEIKKYV	297
Db	266	OSGRKGADIMTGVIDCMRWKITRFREDGEKAPFKGMSVNLRGMGAPLVLIYDEIKKYI	323

RESULT 13

ID	ABG15423	standard; Protein; 325 AA.
XX		
AC	ABG15423;	
XX		
DT	18-FEB-2002	(first entry)
XX		
DE	Novel human diagnostic protein #15414	

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX Homo sapiens.
XX WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI: 2001-639362/73.
XX N-PSDB: AAS79610.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 20; SEQ ID NO 45782; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (I.). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 325 AA:
SQ
Query Match 83.4%; Score 1294.5; DB 22; Length 325;
Best Local Similarity 83.4%; Pred. No. 7.3e-143;
Matches 251; Conservative 19; Mismatches 26; Indels 5; Gaps 4;

OY 237 MMQSGKRGADIMYTCTVDCMKRIADKGAFFKAGSNVLRGCGAFVLVLYD-EIKK 295
|||
DB 264 EXMOSGRKGTIDIMYTCTLDCKWRKIARDKGAFFKAGSNVLRGCGAFVLVLYEXKSKK 323
OY 296 Y 296
DB 324 Y 324
RESULT 14
ABB66082
ID ABB66082 standard; Protein; 299 AA.
AC ABB66082;
DT 26-MAR-2002 (first entry)
XX Drosophila melanogaster polypeptide SEQ ID NO 25038.
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US09231.
XX 23-MAR-2000; 2000US-191637P.
XX 11-JUL-2000; 2000US-0614150.
XX (PEKE) PE CORP NY.
PI Venter JC, Adams M, Li PMD, Myers EW;
DR WPI: 2001-656860/75.
DR N-PSDB: ABL10185.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Disclosure; SEQ ID NO 25038; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX (AB57737-AB872072).
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 299 AA:
SQ
Query Match 79.9%; Score 1241; DB 22; Length 299;
Best Local Similarity 79.7%; Pred. No. 1.2e-136;
Matches 232; Conservative 26; Mismatches 33; Indels 0; Gaps 0;

Db	127	ATSLCFEYVPLDPAFRIRLADDTGCGGOREFTGLGNCILTKLFKSDGIVGLRGFEVSQGII	186
Qy	185	IRRAAIFGVYDPAKGLPDPKKNVHIFVSMIAQSVTAVALGLSTPDDYVRRRRMMOSGRK	244
Db	187	IRRAAIFGVYDPAKGLPDPKKNVHIFVSMIAQSVTAVALGLSTPDDYVRRRRMMOSGRK	246
Qy	245	GADIVYTGVDCCWRKIRAKDEGAAPFKGAMSNVLRGGMGAFVYLVDETIK	295
Db	247	ATEVIRKNTLHCWATIAKOGTGAFFKGAFSNILRGTGAFVLYLDEIK	297
RESULT 15			
ID	ABB67300	standard; Protein; 299 AA.	
AC	ABB67300;		
DT	26-MAR-2002	(first entry)	
DE	Drosophila melanogaster polypeptide SEQ ID NO 28692.		
XX			
XX	Drosophila; developmental biology; cell signalling; insecticide;		
XX	pharmaceutical.		
XX	Drosophila melanogaster.		
XX	MO200171042-A2.		
XX	27-SEP-2001.		
XX			
XX	23-MAR-2001; 2001WO-US09231.		
XX			
XX	23-MAR-2000; 2000US-191637P.		
XX	11-JUL-2000; 2000US-0614150.		
XX			
XX	(PEKE) PE CORP NY.		
XX			
XX	Venter JC, Adams M. LI PWD, Myers EW;		
XX	WPI; 2001-6556860/75.		
XX	N-PSDB; ABL11403.		
XX			
XX	New isolated nucleic acid detection reagent for detecting 1000 or more		
XX	genes from Drosophila and for elucidating cell signalling and cell-cell		
XX	interactions -		
XX			
XX	Disclosure: SEQ ID NO 28692; 21pp + Sequence Listing; English.		
XX			
XX	The invention relates to an isolated nucleic acid detection reagent		
XX	capable of detecting 1000 or more genes from Drosophila. The invention is		
XX	useful in developmental biology and in elucidating cell signalling and		
XX	cell-cell interactions in higher eukaryotes for the development of		
XX	insecticides, therapeutics and pharmaceutical drugs. The invention		
XX	discloses genomic DNA sequences (AB101840-AB16175) and the encoded proteins		
XX	sequences (AB101840-AB16175) and the encoded proteins		
XX	(AB101840-AB16175) and the encoded proteins		
XX	sequences (AB101840-AB16175) and the encoded proteins		
XX	The sequence data for this patent did not form part of the printed		
XX	specification, but was obtained in electronic format directly from WIPO		
XX	at ftp.wipo.int/pub/published_pct_sequences.		
XX			
XX	Sequence 299 AA:		

Query Match	79.9%	Score 1241	DB 22	Length 299
Best Local Similarity	79.7%	Pred. Mismatches 136		
Matches 232	Conservative 26	Identical 35	Indels 0	Gaps 0

QY	5	AMSEPLKDELAVAAVAASKTAVAPIERVKYLLQVQHASKOISAEKQYKGIIDCVRIPE	64
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
Db	7	AVGFVKDPAAGISAAVSKTAVAPIERVKYLLQVQHASKISPDQKQKGMVDCFLRIPE	66
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
QY	65	QGFLSFVHGKMLAVTIRPEPTQALNFAFKDKYQDLFLGGVDRHKQFWRYPAGMLASGAAG	124
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	

Db 67 QGFSEFMKGNLANVIRYEPFGALNFARFDKXQYFGLGVDVKNQNGFWRYFAGNLASGGAAG 126

Qy 125 ATSLCEVYPLDPPARTRLADVGRARQREBHGLDGCIITKFSDBGKGLYOGFENVSGOIT 184

Db 127 ATSLCEVYPLDPPARTRLADVGRARQREBHGLDGCIITKFSDBGKGLYOGFENVSGOIT 186

Qy 185 TYRAAYECVYDTANGKMLPDPKNNVHIEFVSMIAOSVYAVAGLISPPPTVYRRMMMSGRK 244

Db 187 TYRAAYECVYDTANGKMLPDPKNNVHIEFVSMIAOSVYAVAGLISPPPTVYRRMMMSGRK 246

Qy 245 GADIVYGTQYVDCMKRIADDEGAKAFKFGAMSVNLRGAGAFVLYLVEIKK 295

Db 247 ATEVYIKNTLHCMAFTIAKQEGTGFYFGKAPSENIILRGAGAFVLYLVEIKK 297

Search completed: November 12, 2002, 16:45:56
Job time : 30.9328 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:44:25 : Search time 11.6405 Seconds
(without alignments)
750.705 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553
Sequence: 1 MGDHMSFLKDFLAGVA...LNGMGAFVLYDEIKKV 297

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6CTUS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/6ackfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1457.5	93.9	298	3	US-08-961-871-10 Sequence 10, App1
2	301	19.4	469	4	US-09-188-930-339 Sequence 339, App
3	291	18.7	447	4	US-09-160-119-4 Sequence 4, App1
4	291	18.7	674	4	US-09-160-119-2 Sequence 2, App1
5	267	17.2	291	4	US-09-501-558-2 Sequence 2, App1
6	238	15.3	320	2	US-08-933-750C-12 Sequence 12, App1
7	238	15.3	320	4	US-09-234-613-12 Sequence 12, App1
8	233.5	15.0	312	4	US-09-142-565-2 Sequence 2, App1
9	227	14.6	299	1	US-08-518-878B-56 Sequence 56, App1
10	227	14.6	299	2	US-08-470-868A-56 Sequence 56, App1
11	227	14.6	309	1	US-08-518-878B-51 Sequence 51, App1
12	227	14.6	309	2	US-08-807-861A-51 Sequence 51, App1
13	227	14.6	309	2	US-08-470-868A-51 Sequence 51, App1
14	227	14.6	309	3	US-08-946-719A-51 Sequence 51, App1
15	227	14.6	309	3	US-08-946-719A-51 Sequence 51, App1
16	227	14.6	311	2	US-08-775-009-33 Sequence 33, App1
17	225	14.5	311	2	US-08-775-009-32 Sequence 32, App1
18	222.5	14.3	308	2	US-08-937-466-2 Sequence 2, App1
19	222.5	14.3	308	2	US-09-172-528-2 Sequence 2, App1
20	222.5	14.3	308	3	US-09-318-199-2 Sequence 2, App1
21	222.5	14.3	308	4	US-09-503-579-2 Sequence 2, App1
22	218.5	14.1	432	2	US-08-937-466-4 Sequence 4, App1
23	218.5	14.1	432	3	US-09-172-528-4 Sequence 4, App1
24	218.5	14.1	432	3	US-09-318-199-4 Sequence 4, App1
25	218.5	14.1	432	4	US-09-503-579-4 Sequence 4, App1
26	208.5	13.4	293	4	US-09-501-558-4 Sequence 4, App1
27	196.5	12.7	307	2	US-08-807-861A-56 Sequence 56, App1

28	196.5	12.7	307	3	US-09-210-681-56 Sequence 56, App1
29	196.5	12.7	307	3	US-08-946-719A-56 Sequence 56, App1
30	193	12.4	303	1	US-08-294-522B-36 Sequence 36, App1
31	192	12.4	303	1	US-08-518-878B-37 Sequence 37, App1
32	192	12.4	303	2	US-08-807-861A-37 Sequence 37, App1
33	192	12.4	303	2	US-08-470-868A-37 Sequence 37, App1
34	192	12.4	303	3	US-09-210-681-37 Sequence 37, App1
35	192	12.4	303	3	US-08-946-719A-37 Sequence 37, App1
36	190.5	12.3	306	5	PCT-US94-09799-1 Sequence 1, App1
37	188.5	12.1	351	2	US-08-933-750C-19 Sequence 19, App1
38	188.5	12.1	351	4	US-09-234-613-19 Sequence 19, App1
39	185.5	11.9	328	4	US-09-068-140A-15 Sequence 15, App1
40	176	11.3	256	2	US-08-937-466-6 Sequence 6, App1
41	176	11.3	256	2	US-09-172-528-6 Sequence 6, App1
42	176	11.3	256	3	US-09-318-199-6 Sequence 6, App1
43	176	11.3	256	4	US-09-503-579-6 Sequence 6, App1
44	176	11.3	312	4	US-09-188-930-142 Sequence 142, App
45	175.5	11.3	289	4	US-09-068-140A-10 Sequence 10, App1

ALIGNMENTS

RESULT 1
US-08-961-871-10
Sequence 10, Application US/08961871
Patent No. 601858
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: Macgregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
City: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-871-10
Query Match 93.9%; Score 1457.5; DB 3; Length 298;
Best Local Similarity 93.6%; Pred. No. 4.1e-161;
Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;
QY 1 MGDHMSFLKDFLAGVA...LNGMGAFVLYDEIKKV 60


```
Db 1 MGDALSLKDFLAGGIAAASKTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVR 60
QY 61 IPKDGFLSFRGNLANVIRFPTQALNFAFKDKYKOLFGLGVBHKKQFMYEPAGNLASG 120
Db 61 IPKDGFLSFRGNLANVIRFPTQALNFAFKDKYKOLFGLGVBHKKQFMYEPAGNLASG 120
QY 121 GAAGATSLCFYPLDFARTRLADVGR--RAQREFHGLDCCIIRKIFKSDGLKGLYGFVNS 179
Db 121 GAAGATSLCFYPLDFARTRLADVGR--RAQREFHGLDCCIIRKIFKSDGLKGLYGFVNS 180
QY 180 VQGIITIAAATFVYDTAKGMLPDKNVHIFVSMIAQSVTAAGLSTPDDTVARRMM 239
Db 181 VQGIITIAAATFVYDTAKGMLPDKNVHIFVSMIAQSVTAAGLSTPDDTVARRMM 240
QY 240 QSGRKADIMVTGVDCAKRIAKDEGAKAFKGSANVLRGMGAFFVLVLYDEIKKY 297
Db 241 QSGRKADIMVTGVDCAKRIAKDEGAKAFKGSANVLRGMGAFFVLVLYDEIKKY 298
```

```
RESULT 2
US-09-188-930-339
; Sequence 339, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Mouse
US-09-188-930-339
```

Query Match 19.4%; Score 301; DB 4; Length 469;
Best Local Similarity 28.9%; Pred. No. 2.4e-26;
Matches 89; Conservative 64; Mismatches 103; Indels 52; Gaps 14;

```
QY 6 WSFLKDFLAGVAASVTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVR----RI 61
Db 187 WRHL---VAGGAGAVSTCTAPLDRLKVLMOV--HASSNNM-----CIYGGFTQM 233
QY 62 PKEOGFLSFRGNLANVIRFPTQALNFAFKDKYKOLFGLGVDR----HKOFMRYFAGN 116
Db 234 IREGGAKSLMNGNGLNIVKIPESAIKFMAYEOKRILV--GSDOETLRIHER----- 283
QY 117 LASGAGATSLCFYPLDFARTRLADVGRRAQREFHGLDCCIIRKIFKSDGLKGLYGF 176
Db 284 LVASLSLGAIAQSSIIYPMELKTRMAL----RTGQYSGMLDCARRILAKGVAFAFKGY 339
QY 177 NVSVQGIITIAAATFVYDTAKGMLPDKNVHIFVSMIAQSVTAAGLSTPDDTVARRMM 227
Db 340 IPNMIGIITPYGIDLAIVETETKTNWLRRAVNSADP--GVFV--LLACGTISSTCGQIAS 395
QY 228 YPDDTVARRMMQSGRKADIMVTGVDCAKRIAKDEGAKAFKGSANVLRGMGAFFV- 286
Db 396 YPLALVTRRMQAQSIIEGAPVETMSL--FKQILRTGCAFGLKRLAPNFKVIPAISIS 453
QY 287 LVLYDEIK 294
Db 454 YVYVENLK 461
```

RESULT 3

```
US-09-160-119-4
; Sequence 4, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: KRIFER, STEPHANE
; APPLICANT: SOUCHET, MICHEL
; APPLICANT: BRIIL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 447
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-160-119-4
```

Query Match 18.7%; Score 291; DB 4; Length 447;
Best Local Similarity 27.5%; Pred. No. 3.2e-25;
Matches 80; Conservative 53; Mismatches 136; Indels 22; Gaps 7;

```
QY 12 FLAGVAASVTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVRIPKDGFLSFW 71
Db 104 FGLSSVAGAVATAVYPLDLVKTMMONRSTGVSFVGLMKNSDCKRKVIRYGGFGLY 163
QY 72 RGNLANVIRFPTQALNFAFKDKYKOLFGLGVDRHKKQFMYEPAGNLASGAAGATSLCFV 131
Db 164 RGLLPOLLGVAPEKAIKLTVDNDFRDKFM-----HKQSVPLAEMILLAGCAGGSQYIFT 218
QY 132 YPLDFARTRL--AADV--GRAQREFHGLDCCIIRKIFKSDGLKGLYGFVNSVQGIITIR 187
Db 219 NPLEIVKIRILOVAGEIITGPRVS-----ALSVYRDLGFFGIYKAKACFLRDIIFS 269
QY 188 AAFVGVYDTAKGMLPDKNVHIFVSMIAQSVTAAGLSTPDDTVARRMMQSGRGA 246
Db 270 AIFPCIAHVAVASFRANEGGVSPGSLLAGAIAPASALVTPADVITKR--LOVAAABAG 327
QY 247 DIMYGTVDCAKRIAKDEGAKAFKGSANVLRGMGAFFVLVLYDEIKKY 296
Db 328 QTTYSGVIDCFRKLIREGPKALMKGAGARVRSPPQGVTLVLYELLQRW 378
```

```
RESULT 4
US-09-160-119-2
; Sequence 2, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: KRIFER, STEPHANE
; APPLICANT: SOUCHET, MICHEL
; APPLICANT: BRIIL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 674
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-160-119-2
```

Query Match 18.7%; Score 291; DB 4; Length 674;

Best Local Similarity 27.5%, Pred. No. 6e-25;
Matches 80; Conservative 53; Mismatches 136; Indels 22; Gaps 7;

```

RESULT 5
US-09-558-2
: Sequence 2, Application US/09501558
: Patent No. 6403784
: GENERAL INFORMATION:
: APPLICANT: Turner, C. Alexander Jr.
: APPLICANT: Mathur, Brian
: APPLICANT: Zambrowicz, Brian
: APPLICANT: Sands, Arthur T.
: TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and
: FILE REFERENCE: Lex-0012-USA
: CURRENT APPLICATION NUMBER: US/09/501,558
: CURRENT FILING DATE: 2000-02-09
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 291
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-501-558-2

Query Match      17.2%  Score 267;  DB 4;  Length 291;
Best Local Similarity 28.4%;  Pred. No. 1e-22;
Matches 84;  Conservative 51;  Mismatches 137;  Indels 24;  Gaps 9;

QY      10 KDLFAGAAVAAVSVKTAAPVPIERVKLLLOVQHASKOIS-AEKQYKGIICVVRIPKEQGL 68
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB      7 KPEYVGGGLASTAEGCTFPIDLTKTRLDIQOGOTNDARKFEIYRQRMALAVRIGREGLK 66

QY      69 SFMGNLANLVRIPTQALNFAFKDKYKQLELGCYDRKHQFWRYPAGMLASGAAGATSL 128
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB      67 ALYSGIAPAMLRQASVYGTIKIGTYOSLKRFL--IERPED--ETLPVIVIGGILSGVTS 121

QY      129 CFVVPDLFAPTRLADADVGRRAQREFHGGDCIIRKFEKDGRLGLQGFVNSVQGIITRYA 188
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB      122 TIAPITDLKLRMQA----QSNTIQGGHIGFPMNITIQOEGTRGLKGYSLTQRAAIYVG 177

QY      189 AYFEGYDTAK-----GMLDPKKNVHIFVSMIAQSVTAVAG-LLSYPDFVIRRRMQQS 241
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB      178 VELPVYDITKKNHLLISGLMGDTVYTHLFSF-----TCGLAGALAINSPVDVVRTMMNR 232

QY      242 G-RKGADIMYGTCDQMKRIAKDEGAKFFKGAWSNVLR-GMGAGFVLYLVDEIK 295
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB      233 VLRGRCGSGYGTIDCLLQITWKNEGFFALYRGEFPMNLRLGPMNIIFVYTEQLKK 288

RESULT 6
RS-08-933-750C-12

```

```

1 Sequence 12 Application US/08933750C
2 Patent No. 5932442
3
4 GENERAL INFORMATION:
5 APPLICANT: Lal, Preeti
6 APPLICANT: Hillman, Jennifer L.
7 APPLICANT: Bandman, Olga
8 APPLICANT: Shah, Purvi
9 APPLICANT: Au-Young, Janice
10 APPLICANT: Yue, Henry
11 APPLICANT: Guegler, Karl J.
12 APPLICANT: Corley, Neil C.
13 TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
14 NUMBER OF SEQUENCES: 98
15
16 CORRESPONDENCE ADDRESS:
17 ADDRESSEE: Incyte Pharmaceuticals, Inc.
18 STREET: 3174 Porter Drive
19 CITY: Palo Alto
20 STATE: CA
21 COUNTRY: USA
22 ZIP: 94304
23
24 COMPUTER READABLE FORM:
25 MEDIUM TYPE: Diskette
26 COMPUTER: IBM Compatible
27 OPERATING SYSTEM: DOS
28 SOFTWARE: FastSeq for Windows Version 2.0
29 CURRENT APPLICATION DATA:
30 APPLICATION NUMBER: US/08/933.750C
31 FILING DATE: September 23, 1997
32 CLASSIFICATION: 536
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER:
35 FILING DATE:
36 ATTORNEY/AGENT INFORMATION:
37 NAME: Billings, Lucy J.
38 REGISTRATION NUMBER: 36,749
39 REFERENCE/DOCKET NUMBER: PF-0356 US
40 TELECOMMUNICATION INFORMATION:
41 TELEPHONE: 415-855-0555
42 TELEFAX: 415-845-4166
43 TELEX:
44
45 INFORMATION FOR SEQ ID NO: 12:
46 SEQUENCE CHARACTERISTICS:
47 LENGTH: 320 amino acids
48 TYPE: amino acid
49 STRANDEDNESS: single
50 TOPOLOGY: linear
51 IMMEDIATE SOURCE:
52 LIBRARY: SPLNN0702
53 CLONE: 207452
54
55 US-08-933-750C-12

```

[illegible]

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-518-878B-56

Query Match 14.6%; Score 227; DB 1; Length 299;
Best Local Similarity 23.8%; Pred. No. 4,8e-18;
Matches 70; Conservative 52; Mismatches 148; Indels 24; Gaps 7;

QY 12 FLAGAANAASVTAAPIERVKLLQVNHASK--QISAEOYKGIIDCVRIPIKBOGFL 68
DB 7 FLGAGTAACIADLITPELPDTAKVRLQIGESQGPVATVSAQYRGVWGTLTIVWREGR 66
QY 69 SPFRGULANVIRFPYQALNFAFKDKYKQLFLGCVNRHKOFRYFNGNLASGCAATSL 128
DB 67 SLVNGVLAVAGLQROMSFASVRIGLYDSVKQFYTKGSEHAS-----IGSRLLAGSTGALAV 121
QY 129 CFVYPLDFARTRIADAVGRRAQREFHGLDCIIFKSDGLRGLYGFNVSGGIIYRA 188
DB 122 AVAOPTDVAVKVRQAOARAGGRRYOSTVNAVYKTIAREGFRGLMGTSFNVARNAIYVC 181
QY 189 AFGVYDTAK-----GMLDPKKNVHIFVSMIAOSVTAVAGLLSPFPTVRRRRMMOSG 242
DB 182 AELVTYDLKDALKANLMTDLPCH-FTSAGFAGCTTV---IASPVDVVKTRYM----- 233
QY 243 RKGADIMYGTVDQCMRKIKADEGAKAFPGAMSNVLR-GMGCAFVLYLDEIK 295
DB 234 -NSALGOYSSAGHCALTMLQKEGPRAFYKGFMPFLRLGSMNVVMVETYEQLKR 286

RESULT 10
US-08-470-868A-56
Sequence 56, Application US/08470868A
Patent No. 5661485
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-470-868A-56

Query Match 14.6%; Score 227; DB 2; Length 299;
Best Local Similarity 23.8%; Pred. No. 4,8e-18;
Matches 70; Conservative 52; Mismatches 148; Indels 24; Gaps 7;

QY 12 FLAGAANAASVTAAPIERVKLLQVNHASK--QISAEOYKGIIDCVRIPIKBOGFL 68
DB 7 FLGAGTAACIADLITPELPDTAKVRLQIGESQGPVATVSAQYRGVWGTLTIVWREGR 66
QY 69 SPFRGULANVIRFPYQALNFAFKDKYKQLFLGCVNRHKOFRYFNGNLASGCAATSL 128
DB 67 SLVNGVLAVAGLQROMSFASVRIGLYDSVKQFYTKGSEHAS-----IGSRLLAGSTGALAV 121
QY 129 CFVYPLDFARTRIADAVGRRAQREFHGLDCIIFKSDGLRGLYGFNVSGGIIYRA 188
DB 122 AVAOPTDVAVKVRQAOARAGGRRYOSTVNAVYKTIAREGFRGLMGTSFNVARNAIYVC 181
QY 189 AFGVYDTAK-----GMLDPKKNVHIFVSMIAOSVTAVAGLLSPFPTVRRRRMMOSG 242
DB 182 AELVTYDLKDALKANLMTDLPCH-FTSAGFAGCTTV---IASPVDVVKTRYM----- 233
QY 243 RKGADIMYGTVDQCMRKIKADEGAKAFPGAMSNVLR-GMGCAFVLYLDEIK 295
DB 234 -NSALGOYSSAGHCALTMLQKEGPRAFYKGFMPFLRLGSMNVVMVETYEQLKR 286

RESULT 11
US-08-518-878B-51
Sequence 51, Application US/08518878B
Patent No. 5702902
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-518-878B-51

Query Match 14.6%; Score 227; DB 1; Length 309;
Best Local Similarity 23.8%; Pred. No. 5e-18;
Matches 70; Conservative 52; Mismatches 148; Indels 24; Gaps 7;

QY 12 FLAGAANAASKTAVADIERVKLLQVOHASK--QISAERQYKGIIDCVRIKPEOGFL 68
17 FLAGGTACACIDLTFLPDIAKVLQIGESQGVRAVTSQNGYGVGTLITWRTGPR 76
QY 69 SFMGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKKQWRYFAGNLAGSAGATSL 128
77 SLVNGLVAGLOROMSFASVIRGLDYSVKQFYTKGSEHAS-----IGSRLLAGSTTGALAV 131
QY 129 CFVVPLEPAPRLADYGRRAQREFHGLDCIIFPKSDGLRGLYOGFNVSOGIITRYA 188
132 AVAOPDTPVVKRFQARAGGGRKOSTVNAKYTIAREGFRGLMGTSPVARNATVNC 191
QY 189 AYFGVYDTAK-----GMLPDPKNVHIFVSMIAOSTYAVAGLSYFEDVRRMMQSG 242
192 AELTYDLIKALKLANLMTDLPCH-FTSAFAGGCTTV---IASPVDVVKTRYM---- 243
QY 243 RKGDIMYTGTVDCWRKIADKDEKAKAPFKGMSVLR-GMGCAVLYLYDEIK 295
244 -NSALGOYSAGHCALTMLOKEGPRAFYKGMPSFLRLGSMNVVMFYTYEOLKR 296

RESULT 12
US-08-807-861A-51
Sequence 51, Application US/08807861A
Patent No. 5853975
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,861A
FILING DATE: 26-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/518,878

FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-807-861A-51

Query Match 14.6%; Score 227; DB 2; Length 309;
Best Local Similarity 23.8%; Pred. No. 5e-18;
Matches 70; Conservative 52; Mismatches 148; Indels 24; Gaps 7;

QY 12 FLAGAANAASKTAVADIERVKLLQVOHASK--QISAERQYKGIIDCVRIKPEOGFL 68
17 FLAGGTACACIDLTFLPDIAKVLQIGESQGVRAVTSQNGYGVGTLITWRTGPR 76
QY 69 SFMGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKKQWRYFAGNLAGSAGATSL 128
77 SLVNGLVAGLOROMSFASVIRGLDYSVKQFYTKGSEHAS-----IGSRLLAGSTTGALAV 131
QY 129 CFVVPLEPAPRLADYGRRAQREFHGLDCIIFPKSDGLRGLYOGFNVSOGIITRYA 188
132 AVAOPDTPVVKRFQARAGGGRKOSTVNAKYTIAREGFRGLMGTSPVARNATVNC 191
QY 189 AYFGVYDTAK-----GMLPDPKNVHIFVSMIAOSTYAVAGLSYFEDVRRMMQSG 242
192 AELTYDLIKALKLANLMTDLPCH-FTSAFAGGCTTV---IASPVDVVKTRYM---- 243
QY 243 RKGDIMYTGTVDCWRKIADKDEKAKAPFKGMSVLR-GMGCAVLYLYDEIK 295
244 -NSALGOYSAGHCALTMLOKEGPRAFYKGMPSFLRLGSMNVVMFYTYEOLKR 296

RESULT 13
US-08-470-868A-51
Sequence 51, Application US/08470868A
Patent No. 5861485
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.

```

:
:      REGISTRATION NUMBER: 30,742
:      REFERENCE/DOCKET NUMBER: 7853-0031-9999
:
:      TELECOMMUNICATION INFORMATION:
:
:      TELEPHONE: (212) 790-9090
:      TELEFAX: (212) 869-8864
:      TELEX: 66441 PENNIE
:
:      INFORMATION FOR SEQ ID NO: 51:
:
:      SEQUENCE CHARACTERISTICS:
:
:      LENGTH: 309 amino acids
:      TYPE: amino acid
:      STRANDEDNESS: single
:      TOPOLOGY: unknown
:
:
: OS-08-470-868A-51

```

Query Match	14.6%	Score 227	DB 2	Length 309
Best Local Similarity	23.8%	Pred. No.	5e-18	
Matches 70	Conservative 52	Mismatches 148	Indels 24	Gaps 7

[illegible]

RESULT 14
US-09-210-681-51
Sequence 51, Application US/09210681
Patent No. 6057109
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITILE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994

```

1  ATTORNEY/AGENT INFORMATION:
2  NAME: Coruzzi, Laura A.
3  REGISTRATION NUMBER: 30,742
4  REFERENCE/DOCKET NUMBER: 7853-066
5  TELECOMMUNICATION INFORMATION:
6  TELEPHONE: (212) 790-5090
7  TELEFAX: (212) 869-9741/8864
8  TELEX: 66141 PENNIE
9  INFORMATION FOR SEQ ID NO: 51:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 309 amino acids
12 TYPE: amino acid
13 STRANDEDNESS: single
14 TOPOLOGY: unknown
15
16 US-09-210-661-51

```

Query Match	14.6%	Score 227	DB 3	Length 309
Best Local Similarity	23.8%	Pred. No. 5e-18		
Matches 70	Conservative 52	Mismatches 148	Indels 24	Gaps 7

QY	12	FLAGVAANAASVTAAPLPIERVKLLLOVONJASK----	OISEKYOYKGIIDCVIRIPKROGL	68
QY	17	FLGACTAACIADLIFPLDITAKVRKQIOGESGPPRATYS	SAQIRGVMGIIILMVRREGRR	76
QY	69	SFWRCNLANVIRYEPFOALNFAEKDKYKQOLFAGV	DNRKQFMRVYFAGNIIASGGAATSL	128
Db	77	SLYNGLVAGLOROMSPFASVRIGLYSVKVOFYK	SGEHS-----IGSRLIASSTTGALAV	131
QY	129	CFVYVLDPAARTPLADVGRNORREHGLGDCI	IKIFKSPGLRGVGVFNVSVOGIITVAA	168
Db	132	AVAOPTDVVKKRFQOARAGGGRKYOSTVYN	AKTTIAREGEGFGLMGISPPNARNAIYVC	191
QY	189	AYFGVYDTAK-----GMLPDKNVHIFVSN	IAOSVTAVAAILSYFEDTVERRRMOSG	242
Db	192	AEIYVYDILIKDALLKANILMTDILPCH-	FTSAGAGCFCTV---IASPVDVVKTRYA----	243
QY	243	RKGADIMTGYDCKRKITAKDGAANAFFEGANS	VNLVR-GMGCAFVLYLYLDELTK	295
Db	244	NSALGQVSSAGHCALYMLQKEGPRAFYV	GGFMPSELRILGSMNVNMEVYTEQLK	296

RESULT 15
 US-08-946-719A-51
 Sequence 51, Application US/08946719A
 Patent No. 6121017
 GENERAL INFORMATION:
 APPLICANT: Tartaglia, Louis A.
 TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
 TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/946.719A
 FILING DATE: 8-OCT-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/807,861
 FILING DATE: 26-FEB-1997
 APPLICATION NUMBER: US 08/518,878
 FILING DATE: 23-AUG-1995
 APPLICATION NUMBER: US 08/470,868
 FILING DATE: 06-JUN-1995

QY 181 GGIITTAAYGCVYDTAKGMLPDPKNVHIFVSMIAOSVTAAGLSTYPTVRRMMQ 240
 |||||
 Db 181 GGIITTAAYGCVYDTAKGMLPDPKNVHIFVSMIAOSVTAAGLSTYPTVRRMMQ 240
 |||||
 QY 241 SGRKGADIMYGTVDCKRKIAKDEGAKAFKFGAMSNTVLRGAGAFVLYLDEIKKYV 297
 |||||
 Db 241 SGRKGADIMYGTVDCKRKIAKDEGAKAFKFGAMSNTVLRGAGAFVLYLDEIKKYV 297

RESULT 2

US-09-644-31
 ; Sequence 31, Application US/09810644
 ; Patent No. US20020012992A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Clevenger, William
 ; APPLICANT: Wiley, Sandra Eileen
 ; APPLICANT: Willey, Scott W.
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Moos, Walter H.
 ; APPLICANT: Pel, Yezhong
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 ; FILE REFERENCE: 660088.420D3
 ; CURRENT APPLICATION NUMBER: US/09/810,644
 ; CURRENT FILING DATE: 2001-03-14
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 31
 ; LENGTH: 297
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-810-644-31

Query Match 100.0%; Score 1553; DB 10; Length 297;
 Best Local Similarity 100.0%; Pred. No. 1.9e-154;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHAWSLKDFLAGAANAASKTAVAPIERVKLLQVHASKOISAEKQYKGIIDCVR 60
 |||||
 Db 1 MGDHAWSLKDFLAGAANAASKTAVAPIERVKLLQVHASKOISAEKQYKGIIDCVR 60
 |||||
 QY 61 IPKDEGLSEFWKGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHOFWRFAGNLASG 120
 |||||
 Db 61 IPKDEGLSEFWKGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHOFWRFAGNLASG 120
 |||||
 QY 121 GAAGATSLCFEYYPIDFARTRLAADVGRRAOREFHGLGDCIIRKFSDDLRLGYGFNVSV 180
 |||||
 Db 121 GAAGATSLCFEYYPIDFARTRLAADVGRRAOREFHGLGDCIIRKFSDDLRLGYGFNVSV 180
 |||||
 QY 181 GGIITTAAYGCVYDTAKGMLPDPKNVHIFVSMIAOSVTAAGLSTYPTVRRMMQ 240
 |||||
 Db 181 GGIITTAAYGCVYDTAKGMLPDPKNVHIFVSMIAOSVTAAGLSTYPTVRRMMQ 240
 |||||
 QY 241 SGRKGADIMYGTVDCKRKIAKDEGAKAFKFGAMSNTVLRGAGAFVLYLDEIKKYV 297
 |||||
 Db 241 SGRKGADIMYGTVDCKRKIAKDEGAKAFKFGAMSNTVLRGAGAFVLYLDEIKKYV 297

RESULT 3

US-09-811-094-32
 ; Sequence 32, Application US/09811094
 ; Patent No. US2001004414A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Clevenger, William
 ; APPLICANT: Willey, Sandra Eileen
 ; APPLICANT: Willey, Scott W.
 ; APPLICANT: Szabo, Tomas R.

; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Moos, Walter H.
 ; APPLICANT: Pel, Yezhong
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 ; FILE REFERENCE: 660088.420D4
 ; CURRENT APPLICATION NUMBER: US/09/811,094
 ; CURRENT FILING DATE: 2001-03-14
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 32
 ; LENGTH: 298
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-811-094-32

Query Match 89.6%; Score 1391.5; DB 10; Length 298;
 Best Local Similarity 88.6%; Pred. No. 1.3e-137;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHAWSLKDFLAGAANAASKTAVAPIERVKLLQVHASKOISAEKQYKGIIDCVR 60
 |||||
 Db 1 MGDHAWSLKDFLAGAANAASKTAVAPIERVKLLQVHASKOISAEKQYKGIIDCVR 60
 |||||
 QY 61 IPKDEGLSEFWKGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHOFWRFAGNLASG 120
 |||||
 Db 61 IPKDEGLSEFWKGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHOFWRFAGNLASG 120
 |||||
 QY 121 GAAGATSLCFEYYPIDFARTRLAADVGRRAOREFHGLGDCIIRKFSDDLRLGYGFNVSV 179
 |||||
 Db 121 GAAGATSLCFEYYPIDFARTRLAADVGRRAOREFHGLGDCIIRKFSDDLRLGYGFNVSV 180
 |||||
 QY 180 VGGIITTAAYGCVYDTAKGMLPDPKNVHIFVSMIAOSVTAAGLSTYPTVRRMMQ 239
 |||||
 Db 180 VGGIITTAAYGCVYDTAKGMLPDPKNVHIFVSMIAOSVTAAGLSTYPTVRRMMQ 240
 |||||
 QY 240 QSGRKGADIMYGTVDCKRKIAKDEGAKAFKFGAMSNTVLRGAGAFVLYLDEIKKYV 296
 |||||
 Db 240 QSGRKGADIMYGTVDCKRKIAKDEGAKAFKFGAMSNTVLRGAGAFVLYLDEIKKYV 297

RESULT 4

US-09-810-644-32
 ; Sequence 32, Application US/09810644
 ; Patent No. US20020012992A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Clevenger, William
 ; APPLICANT: Wiley, Sandra Eileen
 ; APPLICANT: Willey, Scott W.
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Moos, Walter H.
 ; APPLICANT: Pel, Yezhong
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 ; FILE REFERENCE: 660088.420D3
 ; CURRENT APPLICATION NUMBER: US/09/810,644
 ; CURRENT FILING DATE: 2001-03-14
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 32
 ; LENGTH: 298
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-810-644-32

Query Match 89.6%; Score 1391.5; DB 10; Length 298;
 Best Local Similarity 88.6%; Pred. No. 1.3e-137;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHAWSLKDFLAGAANAASKTAVAPIERVKLLQVHASKOISAEKQYKGIIDCVR 60

Db	1	MTDAALSFARQFLGAGAAALSKTAAVPIERVKLLLOVHASKITADKOYKGIITDCVRR	60
Oy	61	IPKRGSLSPFMRGLAVNIRPEPQALNPAFPKOKYKOLFGLGVDRHNOFRPYFGNLSG	120
Db	61	IPKDEVLSPFRKGLAVNIRPEPQALNPAFKDKYKOLFGLGVDRKQPFMYFEGNLSG	120
Oy	121	GAAGATSLCEVYPLDFASTRILAADVRR-AQREFHGLGDCITIKTEKSDGLRGLOYGENVS	179
Db	121	GAAGATSLCEFYPLDFASTRILAADVAGACAGERERFGLDGCIYKTKSDGKGLTQGFNVS	180
Oy	180	VGGIITIRAAAFGVYDPAKGLPPKKVNHIVFSNMIAIOSYTAVAVGLLSYDPDTRFRPM	239
Db	181	VGGIITIRAAAFGLYDPAKGLPPKNTHTIYISMIMQYTAVAVGLLSYDPDTRFRPM	240
Oy	240	QSGRKGADIMTYGVDCMRKTAKEGAKAPFKGMSVNLGMSGAFVLVLTDETKY	296
Db	241	QSGRKGADIMTYGLDWCVRKTAKEGAKAPFKGMSVNLKMGGAFLVLTDETKY	297

```

RESULT 5
US-09-811-094-33
: Sequence 33, Application US/09811094
: Patent No. US20010044144A1
: GENERAL INFORMATION:
: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.
: APPLICANT: Clevenger, William
: APPLICANT: Willey, Sandra Eileen
: APPLICANT: Willey, Scott W.
: APPLICANT: Szabo, Tomas R.
: APPLICANT: Ghosh, Soumitra S.
: APPLICANT: Moos, Walter H.
: APPLICANT: Pel, Yazhong
: TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT)
: TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
: FILE REFERENCE: 660068.420D4
: CURRENT APPLICATION NUMBER: US/09/811,094
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 33
: LENGTH: 298
: TYPE: PRT
: ORGANISM: Homo sapien
: US-09-811-094-33

```

Query Match	89.28;	Score 1385.5;	DB 10;	Length 298;
Best Local Similarly	87.28;	Pred. No. 5.5e-137;		
Matches 260;	Conservative 21;	Mismatches 16;	Indels 1;	Gaps 1.

[illegible]

RESULT 6

```

US-09-810-644-33
; Sequence 33, Application US/09810644
; Patent No. US20020012992A1
;
GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Thomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yashong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (AMT),
; TITLE OF INVENTION: NOVEL AMT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.42D03
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-33

Query Match      89.2%; Score 1385.5; DB 10; Length 298;
Best Local Similarity 87.2%; Prcd. No. 5.5e-137;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

```

```
QY      1 MEDHASTKPLDLGVAANAASKTAVAPIEVRKLLLOVHAHSKOISAEKKYGITDVCVR   60
        | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 MFEQAISTAKDFLAGGIAAISKRTAVAPIEVKKLLLOYHAHSKOIADDKYKGIYDCIVR   60
QY      61 IPKEGGELSEWNGILANVIKYEPFOALNEAFKDKYKOLFLGAGVDHRHKOFMRYPAGNLASG   120
        | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61 IPKEGGVLSFPMGNLANVIKYRFPTOALNEAFKDKKYOIFLGAQVDKHQOFMRYPAGNLASG   120
QY      121 GAAGATSLCFPVYPLDFAFTRLAADVGRR - AQRERHGIGDCITIKIFEKSDGIRGLGYOGFNVS   179
        | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      121 GAAGATSLCFPVYPLDFAFTRLAADVGKSGSTERERGRGLDDCLVKITTKSKDGIRGLYQGSFVS   180
QY      180 VGGIIIVRAAYFGVYDTAKGMLPDPKNVHFVSMIAIOSVTAAVAGLSITSPEDTVRRMMM   239
        | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      181 VGGIIIVRAAYFGVYDTAKGMLPDPKNTHIVYSNMIAQOTVAIVAGVSYSPEDTVRRMMM   240
QY      240 QSGRGAGDIMTYGVTDCAKRRTAKDEGAAGAFAFKGAMSNVLRMGCAFVLVLYLDELKRVY   297
        | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      241 QSGRGAGAIMTYGTVDCAWRKTJFEREGCGAFAFKGAMSNVLRMGCAFVLVLYLDELKRYI   298
```

```

RESULT 7
US-09-801-368-252
; Sequence 252, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Call, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amlr
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801.368
; CURRENT FILING DATE: 2001-03-07

```

;; PRIOR APPLICATION NUMBER: US 09/487,558
;; PRIOR FILING DATE: 2000-01-19
;; PRIOR APPLICATION NUMBER: US 60/160,587
;; PRIOR FILING DATE: 1999-10-20
;; NUMBER OF SEQ ID NOS: 440
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 252
;; LENGTH: 318
;; TYPE: PRF
;; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-252

Query Match 47.3%; Score 734; DB 10; Length 318;
Best Local Similarity 53.2%; Pred. No. 4.9e-69;

Matches 156; Conservative 45; Mismatches 82; Indels 10; Gaps 5;

QY 7 SFLKDLGAGVAAVSTAAPIERVKLLQVQ-HASKQISAERKQYGIIDCVRRPEKQ 65
DB 22 NPLIDFLMGVSAVAAVSTAAPIERVKLLQVQDEMILKSGRLSHPKGIGECSPRTVKDE 81
QY 66 GFLSPWGNLANVIRYPTQALNFAFKDKYKOLFLGVDHRHKOFRYFAGNLASGAGA 125
DB 82 GVISFWRGNLANVIRYPTQALNFAFKDKIKAMF--GFKKEGAYAKKFAGNLASGAGA 139
QY 126 TSLCFVYPLDFAIRLAD--VGRRAREFHGLDCTIIFKSDGLRGLYOGFNVSOG 182
DB 140 LSLFLVYSLDVARTRLANADSKSKGGAQFNGLIDVYKKTLSQDVAGLGRFLPSVYG 159
QY 183 IIRYRAVFGVYDPAKMLDPKVNHFV--SMIAQSVTAAGLISVPTVRMMMS 241
DB 200 IIVYRGILFMYSLKPLTLTGSLEGSFLSLGVVYTTGASTCSTPDLVRRMMMS 259
QY 242 GRKGADIMYGTGVCWRIKADGAKAFKGAWSNVLRGAGFVLVYDEIK 294
DB 260 GQA---VKYDGAQDCLKRIYAEGVSLFRKGCANILRGVAGVISMVQLQ 309

RESULT 8
US-09-734-569-170
; Sequence 170, Application US/09734569
; Patent No. US20020064816A1
; GENERAL INFORMATION:
; APPLICANT: Lercel, Jens
; APPLICANT: Renz, Andreas
; APPLICANT: Ehrhardt, Thomas
; APPLICANT: Reinold, Andreas
; APPLICANT: Cirpus, Petra
; APPLICANT: Bischoff, Friedrich
; APPLICANT: Frank, Markus
; APPLICANT: Freund, Annette
; APPLICANT: Duwenig, Elke
; APPLICANT: Schmidt, Ralf-Michael
; APPLICANT: Reski, Ralf
; TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
; FILE REFERENCE: BASF-NAE-1332-99-US
; CURRENT APPLICATION NUMBER: US/09/734,569
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/171,101
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.1/WordPerfect 6.1
; SEQ ID NO 170
; LENGTH: 386
; TYPE: PRF
; ORGANISM: Physcomitrella patens
US-09-734-569-170

Query Match 47.3%; Score 734; DB 10; Length 386;
Best Local Similarity 52.9%; Pred. No. 6.2e-69;

Matches 156; Conservative 43; Mismatches 84; Indels 12; Gaps 6;

QY 7 SFLKDLGAGVAAVSTAAPIERVKLLQVQ-HASKQISAERKQYGIIDCVRRPEKQ 65

DB 84 SFWTDFLMGVSAVAAVSTAAPIERVKLLQVQDEMILKSGRLSHPKGIGECSPRTVKDE 143
QY 66 GFLSPWGNLANVIRYPTQALNFAFKDKYKOLFLGVDHRHKO-FWRYFAGNLASGAGA 124
DB 144 GMSLWGNLANVIRYPTQALNFAFKDKYKSLF--GYKKDKGYKKWRGNLASGAGA 201
QY 125 ATSLCFVYPLDFAIRLADVGRR--AQRREFHGLDCTIIFKSDGLRGLYOGFNVS 180
DB 202 ASSLFLVYSLDVARTRLANADSKSKGGERQNGLVYKKTLANIDGAGLGRFAISG 261
QY 181 OGITTYRAVFGVYDPAK--MLPDPKVNHFVSMIAQSVTAAGLISVPTVRMMMS 239
DB 262 AGIIVYRGILFMYSLKPLTLTGSLEGSFLSLGVVYTTGASTCSTPDLVRRMMMS 321
QY 240 QSRKGADIMYGTGVCWRIKADGAKAFKGAWSNVLRGAGFVLVYDEIK 294
DB 322 TSGEA---VKYNGSMDAFKQILAKEGAKSLFKGAGANILRAVAGVLSGVDLQ 373

RESULT 9
US-09-925-301-1459
; Sequence 1459, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05892
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1459
; LENGTH: 132
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (115)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (126)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (129)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1459

Query Match 29.7%; Score 461; DB 10; Length 132;
Best Local Similarity 83.0%; Pred. No. 4.6e-41;

Matches 88; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 1 MGDHMSFLKDLGAGVAAVSTAAPIERVKLLQVQHASKQISAERKQYGIIDCVRR 60
DB 26 MTEQALSFARDFLAGGAAIAISKTAAPIERVKLLQVQHASKQISADKQKIVDCIVR 85
QY 61 IPKEQGLSPWGNLANVIRYPTQALNFAFKDKYKOLFLGVDHRH 106
DB 86 IPKEQGLSPWGNLANVIRYPTQALNFAFKDKYKQFLXGYXKH 131

RESULT 10
US-09-864-761-36440
; Sequence 36440, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:

```

APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aemica-X-1
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIORITY APPLICATION NUMBER: US 60/180,312
PRIORITY FILING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/632,366
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: GB 24263.6
PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
SEQ ID NO 36440
LENGTH: 87
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO L78810.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.3
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
OTHER INFORMATION: SWISSPROT HIT: P05141, EVALU6 6.00e-38
OTHER INFORMATION: EST_HUMAN HIT: AW935235.1, EVALU6 5.00e-37
US-09-864-761-36440

```

	Query Match	25.9%	Score 402.5;	DB 10;	Length 87;	
	Best Local Similarity	87.4%;	Pred. No. 3.4e-35;			
	Matches 76; Conservative	8;	Mismatches 2;	Incls 1;	Gaps 1.	
OY	113 FAGNLASGAAGANSLECYVPPLDEARTRLADVGRR-AOREFHGLDCTIKIFKSDGUNG	171				
				:	:	:
				:	:	:

```

Db          1  FAGNIASGGAAGANTSLCFVYPLDFARTRLADVGKAGAREERFGLDGLVKKYKSDGIKG 60
OY          172  LYGFNFNVSGIIITRYRAAYFGVYDTAK 198
              |||||
Db          61  LYGFNFNVSGIIITRYRAAYFGIYDTAK 87
              |||||

RESULT 11
US-09-777-921A-4
; Sequence 4, Application US/09777921A
; Patent No. US20020115136A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: C0001103
; CURRENT APPLICATION NUMBER: US/09/777, 921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 475
;
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
; US-09-777-921A-4

```

Query Match	22.6%;	Score 350.5;	DB 10;	Length 475;
Best Local Similarity	32.3%;	Pred. No. 7.7e-29;		
Matches	95;	Conservative	55;	Mismatches 115;
			Indels	29;
			Gaps	9;

[illegible]

```

RESULT 12
US-09-777-921A-2
: Sequence 2, Application US/09777921A
: Patent No. US20020115136A1
: GENERAL INFORMATION:
: APPLICANT: MERKULOV et al.
: TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: CLO01103
: CURRENT APPLICATION NUMBER: US/09/777,921A
: CURRENT FILING DATE: 2002-02-07
: NUMBER OF SEQ ID NOS: 126
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 477
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-777-921A-2

```

Best Local Similarity 32.7%, Pred. No. 2e-28;
Matches 96; Conservative 55; Mismatches 116; Indels 27; Gaps 10.

```

RESULT 13
US-09-777-921A-5
: Sequence 5, Application US/09777921A
: Patent No. US2002011516A1
: GENERAL INFORMATION:
: APPLICANT: MERKULOV et al.
: TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: CL001103
: CURRENT APPLICATION NUMBER: US/09/777,921A
: CURRENT FILING DATE: 2002-02-07
: NUMBER OF SEQ ID NOS: 126
: SOFTWARE: FastSeq for Version 4.0
: SEQ ID NO 5
: LENGTH: 410
: TYPE: PRF
: ORGANISM: Homo sapiens
: US-09-777-921A-5

```

Query Match	20.1%;	Score 312;	DB 10;	Length 410;
Best Local Similarly	34.6%;	Pred. No. 6.6e-25;		
Matches 82; Conservative	41;	Mismatches 94;	Indels 20;	Gaps 7;

```

QY 10 KDLFAGNAAVAVSTPAVPIERVLLLOVOHASNQISEKQKIIDCVIRIPEGEFLS 69
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 189 ROLLAGTAGGAGVASTSTAPDLRLKIMOV -HGSK - - -SDKK - -NIEGCFROMVEGSTR 242
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      70 FWRGNLANVIRYPTQALNFAFKDKYKQLEFGVDHRHKQFWRYPAGNLAGSAGAGATSLC 129
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 243 LMRGQTNVIVIAETPAVNAKFWAYQYKKLLTEBQKIGTFPERFISGSM - - -AGATAQT 297
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 130 FVYPLDEPARETLADVGRRAQREFHGLJDCIIKIFKSDGLRGILGYGFNVSVQGIITVRAA 189
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 298 FIVEPWEAKTRRLA - VCKTQG - -YSGIYDCAKRIKTIHGLGCLAFYKGVYVNLGITIYPAGI 353
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 190 YFGYVYDPAK - - -GMLPDPKNVNIHIFVSMHIAQSVTAVAGLLSTPPTDVRRRMMQS 241
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 354 DLAVYEILKSYWLDNFAKDSVNVPGVMWLLGCGALSTSCOGIATSLVPLDLVFRMADQA 410
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT14
US-09-992-598-289
: Sequence 289, Application US/09992598
: Patent No. US20020160384A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Boistein, David

1	APPLICANT:	Desnoyers, Luc
2	APPLICANT:	Eaton, Dan L.
3	APPLICANT:	Ferrara, Napoleone
4	APPLICANT:	Fong, Sherman
5	APPLICANT:	Gerber, Hanspeter
6	APPLICANT:	Gerritsen, Mary E.
7	APPLICANT:	Goddard, Audrey
8	APPLICANT:	Godowski, Paul J.
9	APPLICANT:	Grimaldi, J. Christopher
10	APPLICANT:	Gurney, Austin L.
11	APPLICANT:	Kljavin, Ivar J.
12	APPLICANT:	Napier, Mary A.
13	APPLICANT:	Pan, James
14	APPLICANT:	Paoni, Nicholas F.
15	APPLICANT:	Roy, Margaret Ann
16	APPLICANT:	Stewart, Timothy A.
17	APPLICANT:	Tumas, Daniel
18	APPLICANT:	Watanabe, Colin K.
19	APPLICANT:	Williams, P. Mickey
20	APPLICANT:	Wood, William I.
21	APPLICANT:	Zhang, Zemin
22	TITLE OR INVENTION:	Secreted and Transmembrane Polypeptides and Nucleic
23	TITLE OR INVENTION:	Acids Encoding the Same
24	FILE REFERENCE:	P2730PIC20
25	CURRENT APPLICATION NUMBER:	US/09/992,598
26	CURRENT FILING DATE:	2001-11-14
27	PRIOR APPLICATION NUMBER:	60/049787
28	PRIOR FILING DATE:	1997-06-16
29	PRIOR APPLICATION NUMBER:	60/062250
30	PRIOR FILING DATE:	1997-10-17
31	PRIOR APPLICATION NUMBER:	60/065186
32	PRIOR FILING DATE:	1997-11-12
33	PRIOR APPLICATION NUMBER:	60/065311
34	PRIOR FILING DATE:	1997-11-13
35	PRIOR APPLICATION NUMBER:	60/066770
36	PRIOR FILING DATE:	1997-11-24
37	PRIOR APPLICATION NUMBER:	60/075945
38	PRIOR FILING DATE:	1998-02-25
39	PRIOR APPLICATION NUMBER:	60/078910
40	PRIOR FILING DATE:	1998-03-20
41	PRIOR APPLICATION NUMBER:	60/083322
42	PRIOR FILING DATE:	1998-04-28
43	PRIOR APPLICATION NUMBER:	60/084600
44	PRIOR FILING DATE:	1998-05-07
45	PRIOR APPLICATION NUMBER:	60/087106
46	PRIOR FILING DATE:	1998-05-28
47	PRIOR APPLICATION NUMBER:	60/087607
48	PRIOR FILING DATE:	1998-06-02
49	PRIOR APPLICATION NUMBER:	60/087609
50	PRIOR FILING DATE:	1998-06-02
51	PRIOR APPLICATION NUMBER:	60/087759
52	PRIOR FILING DATE:	1998-06-02
53	PRIOR APPLICATION NUMBER:	60/087827
54	PRIOR FILING DATE:	1998-06-03
55	PRIOR APPLICATION NUMBER:	60/088021
56	PRIOR FILING DATE:	1998-06-04
57	PRIOR APPLICATION NUMBER:	60/088025
58	PRIOR FILING DATE:	1998-06-04
59	PRIOR APPLICATION NUMBER:	60/088026
60	PRIOR FILING DATE:	1998-06-04
61	PRIOR APPLICATION NUMBER:	60/088028
62	PRIOR FILING DATE:	1998-06-04
63	PRIOR APPLICATION NUMBER:	60/088029
64	PRIOR FILING DATE:	1998-06-04
65	PRIOR APPLICATION NUMBER:	60/088030
66	PRIOR FILING DATE:	1998-06-04
67	PRIOR APPLICATION NUMBER:	60/088033
68	PRIOR FILING DATE:	1998-06-04
69	PRIOR APPLICATION NUMBER:	60/088326
70	PRIOR FILING DATE:	1998-06-04
71	PRIOR APPLICATION NUMBER:	60/088167
72	PRIOR FILING DATE:	1998-06-05
73	PRIOR APPLICATION NUMBER:	60/088202

```

1 PRIOR APPLICATION NUMBER: 60/090444
2 PRIOR FILING DATE: 1998-06-24
3 PRIOR APPLICATION NUMBER: 60/090445
4 PRIOR FILING DATE: 1998-06-24
5 PRIOR APPLICATION NUMBER: 60/090472
6 PRIOR FILING DATE: 1998-06-24
7 PRIOR APPLICATION NUMBER: 60/090535
8 PRIOR FILING DATE: 1998-06-24
9 PRIOR APPLICATION NUMBER: 60/090540
10 PRIOR FILING DATE: 1998-06-24
11 PRIOR APPLICATION NUMBER: 60/090542
12 PRIOR FILING DATE: 1998-06-24
13 PRIOR APPLICATION NUMBER: 60/090557
14 PRIOR FILING DATE: 1998-06-24
15 PRIOR APPLICATION NUMBER: 60/090676
16 PRIOR FILING DATE: 1998-06-25
17 PRIOR APPLICATION NUMBER: 60/090678
18 PRIOR FILING DATE: 1998-06-25
19 PRIOR APPLICATION NUMBER: 60/090690
20 PRIOR FILING DATE: 1998-06-25
21 PRIOR APPLICATION NUMBER: 60/090694
22 PRIOR FILING DATE: 1998-06-25
23 PRIOR APPLICATION NUMBER: 60/090695
24 PRIOR FILING DATE: 1998-06-25
25 PRIOR APPLICATION NUMBER: 60/090696
26 PRIOR FILING DATE: 1998-06-25
27 PRIOR APPLICATION NUMBER: 60/090862
28 PRIOR FILING DATE: 1998-06-26
29 PRIOR APPLICATION NUMBER: 60/090863
30 PRIOR FILING DATE: 1998-06-26
31 PRIOR APPLICATION NUMBER: 60/091360
32 PRIOR FILING DATE: 1998-07-01
33 PRIOR APPLICATION NUMBER: 60/091478
34 PRIOR FILING DATE: 1998-07-02
35 PRIOR APPLICATION NUMBER: 60/091544
36 PRIOR FILING DATE: 1998-07-01
37 PRIOR APPLICATION NUMBER: 60/091519
38 PRIOR FILING DATE: 1998-07-02
39 PRIOR APPLICATION NUMBER: 60/091626
40 PRIOR FILING DATE: 1998-07-02
41 PRIOR APPLICATION NUMBER: 60/091633
42 PRIOR FILING DATE: 1998-07-02
43 PRIOR APPLICATION NUMBER: 60/091978
44 PRIOR FILING DATE: 1998-07-07
45 PRIOR APPLICATION NUMBER: 60/091982
46 PRIOR FILING DATE: 1998-07-07
47 PRIOR APPLICATION NUMBER: 60/092182
48 PRIOR FILING DATE: 1998-07-09

```

Query Match	19.68;	Score 304;	DB 9;	Length 469;
Best Local Similarity	29.08;	Pred. No. 5.3e-24;		
Matches 88; Conservative	58;	Mismatches 115;	Indels 42;	Gaps 11

[illegible]

OY 292 EIK 294
: 1
Db 459 NLK 461

RESULT 15
US-09-989-722-289
: Sequence 289, Application US/09989722
: Patent No. US20020072067A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerltisen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730PLC63
: CURRENT APPLICATION NUMBER: US/09/989,722
: PRIOR FILING DATE: 2001-11-19
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/065186
: PRIOR FILING DATE: 1997-11-12
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066770
: PRIOR FILING DATE: 1997-11-24
: PRIOR APPLICATION NUMBER: 60/075945
: PRIOR FILING DATE: 1998-02-25
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/083322
: PRIOR FILING DATE: 1998-04-28
: PRIOR APPLICATION NUMBER: 60/084600
: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/087106
: PRIOR FILING DATE: 1998-05-28
: PRIOR APPLICATION NUMBER: 60/087607
: PRIOR FILING DATE: 1998-06-02
: PRIOR APPLICATION NUMBER: 60/087609
: PRIOR FILING DATE: 1998-06-02
: PRIOR APPLICATION NUMBER: 60/087759
: PRIOR FILING DATE: 1998-06-02
: PRIOR APPLICATION NUMBER: 60/087827
: PRIOR FILING DATE: 1998-06-03
: PRIOR APPLICATION NUMBER: 60/088021
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088025
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088026
: PRIOR FILING DATE: 1998-06-04

: PRIOR APPLICATION NUMBER: 60/088028
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088029
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088030
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088033
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088326
: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088167
: PRIOR FILING DATE: 1998-06-05
: PRIOR APPLICATION NUMBER: 60/088202
: PRIOR FILING DATE: 1998-06-05
: PRIOR APPLICATION NUMBER: 60/088212
: PRIOR FILING DATE: 1998-06-05
: PRIOR APPLICATION NUMBER: 60/088217
: PRIOR FILING DATE: 1998-06-05
: PRIOR APPLICATION NUMBER: 60/088655
: PRIOR FILING DATE: 1998-06-09
: PRIOR APPLICATION NUMBER: 60/088734
: PRIOR FILING DATE: 1998-06-10
: PRIOR APPLICATION NUMBER: 60/088738
: PRIOR FILING DATE: 1998-06-10
: PRIOR APPLICATION NUMBER: 60/088742
: PRIOR FILING DATE: 1998-06-10
: PRIOR APPLICATION NUMBER: 60/088810
: PRIOR FILING DATE: 1998-06-10
: PRIOR APPLICATION NUMBER: 60/088824
: PRIOR FILING DATE: 1998-06-10
: PRIOR APPLICATION NUMBER: 60/088826
: PRIOR FILING DATE: 1998-06-10
: PRIOR APPLICATION NUMBER: 60/088858
: PRIOR FILING DATE: 1998-06-11
: PRIOR APPLICATION NUMBER: 60/088861
: PRIOR FILING DATE: 1998-06-11
: PRIOR APPLICATION NUMBER: 60/088876
: PRIOR FILING DATE: 1998-06-11
: PRIOR APPLICATION NUMBER: 60/089105
: PRIOR FILING DATE: 1998-06-12
: PRIOR APPLICATION NUMBER: 60/089440
: PRIOR FILING DATE: 1998-06-16
: PRIOR APPLICATION NUMBER: 60/089512
: PRIOR FILING DATE: 1998-06-16
: PRIOR APPLICATION NUMBER: 60/089514
: PRIOR FILING DATE: 1998-06-16
: PRIOR APPLICATION NUMBER: 60/089532
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089538
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089598
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089599
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089600
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089653
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089801
: PRIOR FILING DATE: 1998-06-18
: PRIOR APPLICATION NUMBER: 60/089907
: PRIOR FILING DATE: 1998-06-18
: PRIOR APPLICATION NUMBER: 60/089908
: PRIOR FILING DATE: 1998-06-18
: PRIOR APPLICATION NUMBER: 60/089947
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: 60/089948
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: 60/089952
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: 60/090246
: PRIOR FILING DATE: 1998-06-22
: PRIOR APPLICATION NUMBER: 60/090252

```

; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

```

```

Query Match      19.6%; Score 304; DB 10; Length 469;
Best Local Similarity 29.0%; Pred. No. 5.3e-24;
Matches 88; Conservative 58; Mismatches 115; Indels 42; Gaps 11;

```

```

QY 6 WSEFLKDFLAGVAANAASVTAVPERYKLLYOAHASKOISAEKQYGIIDCVIRPKEQ 65
DB 187 WRHL---VAGGAGAVSRTCTAPLDRKLVMOY-HASR-----SNNMGIVGGFTOMIREG 237
QY 66 GFLSFWRGNLANVIRYFFPTQALNFAFKDKYKOLFLGCVDR-----HKQFWRYFAGNLASG 120
DB 238 GARSLWRGNGINVLKIPESAIKFMAYEQIKRLV--GSDQETLRIHER-----LVAG 287

```

```

QY 121 GAAGATSLCFVYPLDARTRLADVGRRORERHGLDCTIKIFKSDGLNGLYQGENVSV 180
DB 288 SLGAGIAOSSIVPEMEVLKTFMAL-----RKTGOYSGMLDCARRILAREGVAAPFKGYVPM 343
QY 181 OGIIYRAAFGYVDPAKGM-----LPDPKNVHIFVSMIAQSVTAAGLSYPEDT 232
DB 344 LGIIPYAGIDLAVYETLKNMLOHYAVNSADP---GVFVLLACGTMSSTGQLASTPLAL 400
QY 233 VRRRMWOSGRKADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFV-LVLYD 291
DB 401 VRTRMQAQASTEGAPEVTMSSL--FKHILRTGAFGLYRGLADNPMKVIIPAVSISVYVE 458
QY 292 EIK 294
DB 459 NLK 461

```

```

Search completed: November 12, 2002, 16:56:55
Job time : 7.31915 secs

```


GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:44:05 ; Search time 13.9686 Seconds
(without alignments)
2044.001 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553
Sequence: 1 MGDHMSFLKDLACAVAA.....LRMGCAFVLYLDEIKKV 297

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR73:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1526.5	98.3	298	1 A44778	ADP,ATP carrier pr
2	1466.5	94.4	298	2 I60173	adenine nucleotide
3	1463.5	94.2	298	1 S37210	ADP,ATP carrier pr
4	1458.5	93.9	298	1 XMBO	ADP,ATP carrier pr
5	1391.5	89.6	298	1 A29132	ADP,ATP carrier pr
6	1385.5	89.2	298	1 S03894	ADP,ATP carrier pr
7	1380.5	88.9	298	2 B43646	ADP,ATP carrier pr
8	1368.5	88.1	298	2 S31814	ADP,ATP carrier pr
9	1142.5	67.3	301	1 S31935	ADP,ATP carrier pr
10	1045.5	67.3	313	2 T25850	hypothetical prote
11	1043.5	67.2	313	2 T23207	hypothetical prote
12	1037.5	66.8	300	2 T25371	hypothetical prote
13	1005.5	64.7	300	2 T15206	hypothetical prote
14	973.5	62.7	339	2 A41677	ADP,ATP carrier pr
15	904.5	58.2	301	2 S51132	ADP,ATP carrier pr
16	772	49.7	306	2 T20012	hypothetical prote
17	770.5	49.6	308	1 S30259	ADP,ATP carrier pr
18	756.5	48.7	387	2 S14876	ADP,ATP carrier pr
19	752.5	48.5	322	2 T40526	ADP,ATP translocas
20	752.5	48.5	386	2 T09709	ADP,ATP carrier pr
21	751.5	48.4	387	2 S16568	ADP,ATP carrier pr
22	746.5	48.1	379	2 T04608	ADP,ATP carrier pr
23	746.5	48.1	382	2 S33630	ADP,ATP carrier pr
24	745.5	48.0	326	2 T25728	hypothetical prote
25	745.5	48.0	386	2 S17917	ADP,ATP carrier pr
26	744.5	47.9	386	2 S21974	ADP,ATP carrier pr
27	740	47.6	379	2 S21313	ADP,ATP carrier pr
28	740	47.6	386	2 S14874	ADP,ATP carrier pr
29	737	47.5	385	1 S29852	ADP,ATP carrier pr

30	736	47.4	307	2 A36582	ADP,ATP carrier pr
31	734	47.3	318	1 A31978	ADP,ATP carrier pr
32	733.5	47.2	313	1 XMNC	ADP,ATP carrier pr
33	729	46.9	305	2 S68154	ADP,ATP carrier pr
34	728.5	46.9	306	2 T42011	ADP,ATP carrier pr
35	718.5	46.3	309	2 A24849	ADP,ATP carrier pr
36	676	43.5	298	2 T24029	hypothetical prote
37	508	32.7	327	2 T51577	ADP,ATP translocas
38	368	23.7	415	2 T48171	hypothetical prote
39	367.5	23.7	325	2 T04273	hypothetical prote
40	363	23.4	381	2 T51158	hypothetical prote
41	350.5	22.6	475	2 T50686	peroxisomal Ca-dep
42	349.5	22.5	352	2 T01729	mitochondrial solu
43	345.5	22.2	358	2 T45934	hypothetical prote
44	334.5	21.5	348	2 D84798	probable mitochond
45	327	21.1	332	2 T47703	Ca-dependent solut

ALIGNMENTS

RESULT 1
A44778
ADP,ATP carrier Protein T1 - human
N:Alternate names: mitochondrial ADP,ATP translocase 1
C:Species: Homo sapiens (man)
C>Date: 17-Mar-2000 #sequence, revision 17-Mar-2000 #text, change 17-Mar-2000
C:Accession: A44778; S03893; A39891; A28116
J:Ref. 1: Warner, C.K.; Hodges, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, R. Biol. Chem. 264, 13998-14004, 1989
A>Title: A human muscle adenine nucleotide translocator gene has four exons, its local
A:Reference number: A44778; MIM:89340499; PMID:2547778
A:Accession: A44778
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-298 <LIA>
A:Cross-references: GB:J04982; NID:q178658; PIDN:AAA51736.1; PID:q178659
R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A>Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATF
A:Reference number: S03893; MIM:89236396; PMID:2541251
A:Accession: S03893
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <CO2>
R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A>Title: CDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a lea
A:Reference number: A39891; MIM:88041149; PMID:2823266
A:Accession: A39891
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15, 'A', 'A', '17-146, 'RR', '149, '151-226, 'U', '228-298 <NEC>
A:Cross-references: GB:J02966; NID:q339919; PIDN:AAA61223.1; PID:q339920
R:Houlsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A>Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in
A:Reference number: A94197; MIM:88124845; PMID:2829183
A:Accession: A28116
A:Molecule type: mRNA
A:Residues: 1-37 <HO>
A:Cross-references: GB:J03593; NID:q339724; PIDN:AAA36751.1; PID:q339725
A:Experimental source: liver
C:Genetics:
A:Gene: GDB:ANTL1, T1
A:Cross-references: GDB:119680; OMIM:103220
A:Map position: 4q35-4q35
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; Transmembrane protein
F:2-298/Product: ADP,ATP carrier protein #status predicted <MAT>
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 98.3%; Score 1526.5; DB 1; Length 298;
Best Local Similarity 98.3%; Pred. No. 1.6e-110;
Matches 293; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGVAAVSKTAVAPIERVKLLQVHSAKQISAEKQKGIIDCVYR 60
D 1 MGDHMSFLKDFLAGVAAVSKTAVAPIERVKLLQVHSAKQISAEKQKGIIDCVYR 60
QY 61 IPKEGGFLSFWRGNLANVIRYFPQALNFAFKDKYKQFLGCVDRHKQFWRYPAGNLASG 120
D 61 IPKEGGFLSFWRGNLANVIRYFPQALNFAFKDKYKQFLGCVDRHKQFWRYPAGNLASG 120
QY 121 GAAGTSLCFYYPIDFARTRLAADYGR-RAOREFHGLDCCIIFKPSDGLGLVGGFNVS 179
D 121 GAAGTSLCFYYPIDFARTRLAADYGR-RAOREFHGLDCCIIFKPSDGLGLVGGFNVS 180
QY 180 VOGIITVRAAFYGYDTRAKGMLPDPKNVHIFVSMIAQSVTAVALGLSYPEPTVRRMM 239
D 181 VOGIITVRAAFYGYDTRAKGMLPDPKNVHIFVSMIAQSVTAVALGLSYPEPTVRRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 297
D 241 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 298

RESULT 2

adenine nucleotide translocator - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999

C:Accession: 160173

R:Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.

Biochim. Biophys. Acta 1152, 192-196, 1993

A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat

A:Reference number: 160173; MUID:94002161; PMID:8399300

A:Accession: 160173

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-298 <RES>

A:Cross-references: EMBL:X61667; NID:9400426; PIDN:CAA43842.1; PID:9400427

C:Genetics:

A:Gene: ancl

A:Introns: 37/3; 200/1; 247/1

C:Superfamily: ADP,ATP carrier protein: ADP,ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.4%; Score 1466.5; DB 2; Length 298;

Best Local Similarity 94.3%; Pred. No. 4.3e-125;

Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGVAAVSKTAVAPIERVKLLQVHSAKQISAEKQKGIIDCVYR 60
D 1 MGDHMSFLKDFLAGVAAVSKTAVAPIERVKLLQVHSAKQISAEKQKGIIDCVYR 60
QY 61 IPKEGGFLSFWRGNLANVIRYFPQALNFAFKDKYKQFLGCVDRHKQFWRYPAGNLASG 120
D 61 IPKEGGFLSFWRGNLANVIRYFPQALNFAFKDKYKQFLGCVDRHKQFWRYPAGNLASG 120
QY 121 GAAGTSLCFYYPIDFARTRLAADYGR-RAOREFHGLDCCIIFKPSDGLGLVGGFNVS 179
D 121 GAAGTSLCFYYPIDFARTRLAADYGR-RAOREFHGLDCCIIFKPSDGLGLVGGFNVS 180
QY 180 VOGIITVRAAFYGYDTRAKGMLPDPKNVHIFVSMIAQSVTAVALGLSYPEPTVRRMM 239
D 181 VOGIITVRAAFYGYDTRAKGMLPDPKNVHIFVSMIAQSVTAVALGLSYPEPTVRRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 297
D 241 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 298

D 241 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 298

RESULT 3

ADP,ATP carrier protein T1 - mouse

N:Alternate names: adenine nucleotide carrier

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999

C:Accession: S37210

R:Laplace, C.; Costet, P.

submitted to the EMBL Data Library, September 1993

A:Reference number: S37210

A:Accession: S37210

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-298 <LAP>

A:Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628

C:Genetics:

A:Gene: ANCL

C:Superfamily: ADP,ATP carrier protein: ADP,ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1463.5; DB 2; Length 298;

Best Local Similarity 94.0%; Pred. No. 8e-125; 7; Indels 1; Gaps 1;

Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGVAAVSKTAVAPIERVKLLQVHSAKQISAEKQKGIIDCVYR 60
D 1 MGDHMSFLKDFLAGVAAVSKTAVAPIERVKLLQVHSAKQISAEKQKGIIDCVYR 60
QY 61 IPKEGGFLSFWRGNLANVIRYFPQALNFAFKDKYKQFLGCVDRHKQFWRYPAGNLASG 120
D 61 IPKEGGFLSFWRGNLANVIRYFPQALNFAFKDKYKQFLGCVDRHKQFWRYPAGNLASG 120
QY 121 GAAGTSLCFYYPIDFARTRLAADYGR-RAOREFHGLDCCIIFKPSDGLGLVGGFNVS 179
D 121 GAAGTSLCFYYPIDFARTRLAADYGR-RAOREFHGLDCCIIFKPSDGLGLVGGFNVS 180
QY 180 VOGIITVRAAFYGYDTRAKGMLPDPKNVHIFVSMIAQSVTAVALGLSYPEPTVRRMM 239
D 181 VOGIITVRAAFYGYDTRAKGMLPDPKNVHIFVSMIAQSVTAVALGLSYPEPTVRRMM 240
QY 240 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 297
D 241 QSGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 298

RESULT 4

ADP,ATP carrier protein T1 - bovine

N:Alternate names: ADP/ATP translocase T1

C:Species: Bos primigenius taurus (cattle)

C:Date: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999

C:Accession: A43646; A24822; A03181; A61343; S69369

R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.

Biochem. Biophys. Res. Commun. 138, 850-857, 1986

A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently

A:Reference number: A43646; MUID:89229093; PMID:2540808

A:Accession: A43646

A:Molecule type: mRNA

A:Residues: 1-298 <POW>

A:Cross-references: GB:M24102; NID:9529414; PIDN:AAA30768.1; PID:9529415

R:Rasmussen, U.B.; Wohlrab, H.

Biochem. Biophys. Res. Commun. 138, 850-857, 1986

A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unus

A:Reference number: A24822; MUID:86295775; PMID:3017341

A:Accession: A24822

A:Molecule type: mRNA

A:Residues: 208-298 <RAS>

A:Cross-references: GB:M13783; MID:g162630; PIDN:AAA30363.1; PID:g162631
 R:Aquila, H.; Mistra, D.; Eulitz, M.; Klingenberg, M.
 Hoppel-Seyler, S. Z. Physiol. Chem. 363, 345-349, 1982
 A:Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria
 A:Reference number: A03181; MUID:82198267; PMID:7076130
 A:Accession: A03181
 A:Molecule type: Protein
 A:Residues: 251,'X','53-70','X','72-109','X','111-298 <A0U>
 A:Note: residue 52 may be methyllysine
 R:Abdel, W.; Wachter, E.; Aquila, H.; Klingenberg, M.
 Biochim. Biophys. Acta 670, 176-180, 1981
 A:Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondria
 A:Reference number: A61343; MUID:82046808; PMID:6271240
 A:Accession: A61343
 A:Molecule type: protein
 A:Residues: 205-298 <BAB>
 R:Oeltmeier, W.; Masson, K.; Kalina, S.
 Eur. J. Biochem. 227, 730-733, 1995
 A:Title: ((3)H)-7-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP/ATP carrier
 A:Reference number: S69369; MUID:95172058; PMID:7867632
 A:Accession: S69369
 A:Molecule type: protein
 A:Residues: 49-63;134-168 <OET>
 C:Comment: This protein is synthesized in the cytosol and transported into the mitochondrion
 C:Complex: homodimer
 C:Function:
 A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP generated during oxidative phosphorylation
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitochondrion; repeat homology
 F:5-99/Domin: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domin: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domin: ADP,ATP carrier protein repeat homology <ACP3>
 F:52/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 93.9%; Score 1458.5; DB 1; Length 298;
 Best Local Similarity 94.3%; Pred. No. 2.3e-124;
 Matches 281; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

Oy 1 MGDHMSLFKQFLGAVAAVSKTAVAPIERVKLLILOVQHSKQISAEKQKGIIDCVR 60
 Db 1 MSDQALSLKQFLGAVAAVSKTAVAPIERVKLLILOVQHSKQISAEKQKGIIDCVR 60
 Oy 61 IPKEGFLSFWRGNLANVIRFPTQALNFAFKDYKQFLGCVGRHKKQFMYRFFAGNLASG 120
 Db 61 IPKEGFLSFWRGNLANVIRFPTQALNFAFKDYKQFLGCVGRHKKQFMYRFFAGNLASG 120
 Oy 121 GAAGTSLCFEYPPDFAFTRLAADYGR-RAQREFHGLGDCITIKFKSGLGLYOGFNVS 179
 Db 121 GAAGTSLCFEYPPDFAFTRLAADYGR-RAQREFHGLGDCITIKFKSGLGLYOGFNVS 180
 Oy 180 VGGIITFAAFCGVYDTAKGMLPDPKNVHIFVSMWIAOSYTAAVAGLSTPDTYRRRMM 239
 Db 181 VGGIITFAAFCGVYDTAKGMLPDPKNVHILYSWMLAQYTAAVAGLSTPDTYRRRMM 240
 Oy 240 QSGRKGADIMYTGIVDCMRKIAKDEGAKAFKFGAMSNVLRMGGAFLVLYDEIKKKY 297
 Db 241 QSGRKGADIMYTGIVDCMRKIAKDEGPKAFKFGAMSNVLRMGGAFLVLYDEIKKKY 298

RESULT 5
 A29132
 ADP,ATP carrier protein T2 - human
 N:Alternate names: mitochondrial ADP,ATP translocase 2
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C:Accession: A29132 C28116
 R:Batistini, R.; Ferrati, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
 J. Biol. Chem. 267, 4355-4359, 1987
 A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulated
 A:Reference number: A29132; MUID:87166056; PMID:3031073
 A:Accession: A29132

A: Molecule type: mRNA
A: Residues: 1-298 <BAV>
A: Cross-references: GB:0202683; NID:q179246; PIDN:AAA35579.1; PID:q179247
R: Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A: Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A: Reference number: A94197; MUID:88124845; PMID:2829183
A: Accession: C28116
A: Molecule type: mRNA
A: Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>
A: Cross-references: GB:003591; NID:q339720; PIDN:AAA36749.1; PID:q339721
A: Experimental source: clone pHA73
C: Genetics:
A: Gene: GDB:ANT2; T3; 2F1
A: Cross-references: GDB:125190; OMIM:300150
A: Map position: Xq13-Xq46
A: Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:ANT1
C: Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
C: Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F: 5-99/domain: ADP/ATP carrier protein repeat homology <ACP1>
F: 110-202/domain: ADP/ATP carrier protein repeat homology <ACP2>
F: 207-298/domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 89.6%; Score 1391.5; DB 1; Length 298;
Best Local Similarity 88.6%; Pred. No. 2.6e-118;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDAHSLKLPFLAGAAVASKTAVAPIEYKLLLOVHNSKQISAEQYKGIIDCVR 60
Db 1 MTDALSPAKKFLAGCAVAAISKTAVAPIEYKLLLOVHNSKQITDADKYKGIIDCVR 60

QY 61 IPKEGCFSPKRGMLNANYIRFPPQALNFAKDKDYKQDLGGVYHROHQPFRYFAGNLASG 120
Db 61 IPKEDEVSPKRGMLNANYIRFPPQALNFAKDKDYKQDLGGVYHROHQPFRYFAGNLASG 120

QY 121 GAAGATSLCFEYPLDFAFTRLADVGR-ADQEFHGLGDCIIKIFKSDGLRGLYGCVNS 179
Db 121 GAAGATSLCFEYPLDFAFTRLADVGR-ADQEFHGLGDCIIKIFKSDGLRGLYGCVNS 180

QY 180 VGGITTYAAAFEGYDTPAKGMLPDPKNVHIFVSMINOSYAVAVGLSYSPDPVRRMM 239
Db 180 VGGITTYAAAFEGYDTPAKGMLPDPKNVHIFVSMINOSYAVAVGLSYSPDPVRRMM 240

QY 240 QSGRKGADIMYTGIVDCWRKIADKDEGAKAFKFGAMSVNLKMGCAFVLVLYDEIKKY 296
Db 240 QSGRKGADIMYTGIVDCWRKIADKDEGAKAFKFGAMSVNLKMGCAFVLVLYDEIKKY 297

RESULT 6
S03894
ADP/ATP carrier protein T3 - human
N: Alternate names: ADP/ATP carrier protein T2 (misidentification); mitochondrial ADP,
C: Species: Homo sapiens (man)
C: Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C: Accession: S03894; B28116
R: Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A: Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
A: Reference number: S03893; MUID:89236396; PMID:2541251
A: Accession: S03894
A: Status: not compared with conceptual translation
A: Molecule type: DNA
A: Residues: 1-298 <COZ>
R: Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A: Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A: Reference number: A94197; MUID:88124845; PMID:2829183
A: Accession: B28116
A: Molecule type: mRNA
A: Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>
A: Cross-references: GB:003592; NID:q339722; PIDN:AAA36750.1; PID:q339723
C: Experimental source: liver
C: Genetics:

A:Gene: GDB:ANT3; ANT3Y
 A:Cross-references: GDB:125184; OMIM:300151; OMIM:403000
 A:Map position: xp22.32-xp22.32; Yp11.3-Yp11.3
 A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:2-298/Product: ADP,ATP carrier protein #status predicted <ACPI>
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACPI>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACPI>

Query Match 89.2%; Score 1385.5; DB 1; Length 298;
 Best Local Similarity 87.2%; Pred. No. 9.1e-118;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVHASKOISAEKQYGIIDCVR 60
 DQ 1 MTEQAIISPAKDFLAGIAAISTKAVAPIERVKLLQVHASKOIAADKQYGIIDCVR 60
 QY 61 IPKEGFLSFWRGNLANVIRFPTQALNFAFKDKYKQFLGVDNRHKOFRYFAGNLASG 120
 DQ 61 IPKEGFLSFWRGNLANVIRFPTQALNFAFKDKYKQFLGVDNRHKOFRYFAGNLASG 120
 QY 121 GAAGATSLCFEYPLDFATRIADVGRR-AOREFHGLGDCIIKIFKSGDLGLYGFNV 179
 DQ 121 GAAGATSLCFEYPLDFATRIADVGRR-SGTEREFGDLGDCIVKITSKGIGLYGFNV 180
 QY 180 VQGIITIRAAFGYVDRAKGLPDPKNVHIFVSMIAOSVTAVALGLSYPEDTYRRRMM 239
 DQ 181 VQGIITIRAAFGYVDRAKGLPDPKNVHIFVSMIAOSVTAVALGLSYPEDTYRRRMM 240
 QY 240 QSGRRGADIMYTGTVDCMRKIAKDEGAKEFKGAMSNVLRMGAFVLYLDEIKKY 297
 DQ 241 QSGRRGADIMYTGTVDCMRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDEIKKY 298

RESULT 7

ADP,ATP carrier protein T2 - bovine
 B43646
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
 C:Accession: B43646
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093; PMID:2540808
 A:Accession: B43646
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <POM>
 A:Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACPI>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACPI>

Query Match 88.9%; Score 1380.5; DB 2; Length 298;
 Best Local Similarity 86.9%; Pred. No. 2.6e-117;
 Matches 259; Conservative 21; Mismatches 17; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVHASKOISAEKQYGIIDCVR 60
 DQ 1 MTEQAIISPAKDFLAGIAAISTKAVAPIERVKLLQVHASKOIAADKQYGIIDCVR 60
 QY 61 IPKEGFLSFWRGNLANVIRFPTQALNFAFKDKYKQFLGVDNRHKOFRYFAGNLASG 120
 DQ 61 IPKEGFLSFWRGNLANVIRFPTQALNFAFKDKYKQFLGVDNRHKOFRYFAGNLASG 120
 QY 121 GAAGATSLCFEYPLDFATRIADVGRR-AOREFHGLGDCIIKIFKSGDLGLYGFNV 179
 DQ 121 GAAGATSLCFEYPLDFATRIADVGRR-SGTEREFGDLGDCIVKITSKGIGLYGFNV 180

QY 180 VQGIITIRAAFGYVDRAKGLPDPKNVHIFVSMIAOSVTAVALGLSYPEDTYRRRMM 239
 DQ 181 VQGIITIRAAFGYVDRAKGLPDPKNVHIFVSMIAOSVTAVALGLSYPEDTYRRRMM 240
 QY 240 QSGRRGADIMYTGTVDCMRKIAKDEGAKEFKGAMSNVLRMGAFVLYLDEIKKY 297
 DQ 241 QSGRRGADIMYTGTVDCMRKILKDEGKAFKFGAMSNVLRMGAFVLYLDEIKKY 298

RESULT 8

ADP,ATP carrier protein T2 - mouse
 S31814
 N:Alternate names: adenine nucleotide translocase
 C:Species: Mus musculus (house mouse)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998
 C:Accession: S31814
 R:Costet, P.; Laplace, C.
 submitted to the EMBL Data Library, January 1993
 A:Reference number: S31814
 A:Accession: S31814
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <COS>
 A:Cross-references: EMBL:X70847
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACPI>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACPI>

Query Match 88.1%; Score 1368.5; DB 2; Length 298;
 Best Local Similarity 87.2%; Pred. No. 3.2e-116;
 Matches 259; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVHASKOISAEKQYGIIDCVR 60
 DQ 1 MTEQAIISPAKDFLAGIAAISTKAVAPIERVKLLQVHASKOIAADKQYGIIDCVR 60
 QY 61 IPKEGFLSFWRGNLANVIRFPTQALNFAFKDKYKQFLGVDNRHKOFRYFAGNLASG 120
 DQ 61 IPKEGFLSFWRGNLANVIRFPTQALNFAFKDKYKQFLGVDNRHKOFRYFAGNLASG 120
 QY 121 GAAGATSLCFEYPLDFATRIADVGRR-AOREFHGLGDCIIKIFKSGDLGLYGFNV 179
 DQ 121 GAAGATSLCFEYPLDFATRIADVGRR-SGTEREFGDLGDCIVKITSKGIGLYGFNV 180
 QY 180 VQGIITIRAAFGYVDRAKGLPDPKNVHIFVSMIAOSVTAVALGLSYPEDTYRRRMM 239
 DQ 181 VQGIITIRAAFGYVDRAKGLPDPKNVHIFVSMIAOSVTAVALGLSYPEDTYRRRMM 240
 QY 240 QSGRRGADIMYTGTVDCMRKIAKDEGAKEFKGAMSNVLRMGAFVLYLDEIKKY 296
 DQ 241 QSGRRGADIMYTGTVDCMRKIAKDEGKAFKFGAMSNVLRMGAFVLYLDEIKKY 297

RESULT 9

ADP,ATP carrier protein - African malaria mosquito
 S31935
 C:Species: Anopheles gambiae (African malaria mosquito)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S31935; S31936
 R:Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H.
 submitted to the EMBL Data Library, February 1993
 A:Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae
 A:Reference number: S31935
 A:Accession: S31935
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-301 <BEA>
 A:Cross-references: EMBL:Z21814; EMBL:Z21815
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:7-101/Domain: ADP,ATP carrier protein repeat homology <ACPI>

Db 68 QGVLSIMRGVNVANVIRYPPQAFNFAFKDYFKNIF-PRYDQNTDESKFPCVNIISGATAG 126
QY 125 AFSLCFVYPLDPARTRLADYGRRAQREFFHGLGDCIIEFKSDGLRGLYOGFNNSVGGII 184
Db 127 AISLIIVYPLDPARTRLASDIDGKGRQFTGIFDCLAKIYKOTGLISLXSGFGVSVTGII 186
QY 185 IYRAAYFGVYDTAKGML-PDPKNVHIEFVSMIAOSVTAVAGILSYPEPTVRRRMMOSGR 243
Db 187 VYRGSYFGLYDSAKALFTNDKNINIVLKMVAQSVTTLAGLISTPEPTVRRRMMMSGR 246
QY 244 KG-ADIMVTGTDCWRKIADDEGAKAFKFGAMSNVLRGMGAFVLYDEIKKYV 297
Db 247 KGKEIQYKNTIDCWIKILRNDEGFGFGKAMANYIRGAGGALVLYFDEIQKLI 301

Search completed: November 12, 2002, 16:48:36
Job time : 14.9686 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:43:20 : Search time 7.6495 Seconds

(without alignments)
1610.364 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553
Sequence: 1 MGDHMSFLKDFLAGAFAA.....LRMGAFVLYDEIKKYV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1526.5	98.3	298	ADP1_HUMAN	P12235 ratu mus sapien
2	1466.5	94.4	298	ADP1_RAT	Q05662 ratu mus norv
3	1463.5	94.2	298	ADP1_MOUSE	P48962 mus musculi
4	1453.5	93.6	297	ADP1_BOVIN	P02722 bos tauris
5	1408.5	90.7	298	ADP2_MOUSE	P51881 mus musculi
6	1407.5	90.6	298	ADP2_RAT	Q09673 ratu mus norv
7	1398.5	90.1	298	ADP2_HUMAN	P05141 homo sapien
8	1385.5	89.2	298	ADP3_HUMAN	P12236 homo sapien
9	1380.5	88.9	298	ADP3_BOVIN	P32007 bos tauris
10	1211	78.0	297	ADP1_DROME	Q26365 drosophila
11	1162.5	74.9	301	ADP1_ANGOA	Q27238 anopheles g
12	973.5	62.7	339	ADP1_CHIKRE	P31692 chikorella k
13	770.5	45.6	308	ADP1_CHIKRE	P27080 chikorella k
14	756.5	48.7	387	ADP1_MAIZE	P04709 zea mays (m
15	752.5	48.5	322	ADP1_SCHPO	Q09188 schizosacch
16	752.5	48.5	386	ADP1_GOSHI	Q22342 gossypium h
17	751.5	48.4	382	ADP1_ORYSA	P31691 oryza sativ
18	751.5	48.4	382	ADP2_MAIZE	P12857 zea mays (m
19	746	48.0	381	ADP1_ARATH	P31167 arabidopsis
20	744.5	47.9	386	ADP1_SOLTU	P25083 solanum tub
21	742.5	47.8	331	ADP1_WHEAT	Q41629 triticum ae
22	740	47.6	386	ADP2_SOLTU	P27081 solanum tub
23	736	47.4	307	ADP3_YEAST	P18238 saccharomyc
24	734	47.3	318	ADP2_YEAST	P18239 saccharomyc
25	733.5	47.2	313	ADP1_NEUCR	P02723 neurospora
26	731	47.1	385	ADP2_ARATH	P40941 arabidopsis
27	729	46.9	305	ADP2_KLULA	P49382 kluyveromyc
28	728.5	46.9	331	ADP2_WHEAT	Q41630 triticum ae
29	718.5	46.3	309	ADP1_YEAST	P04710 saccharomyc
30	302.5	19.5	678	CMC1_HUMAN	O75446 homo sapien
31	300.5	19.3	330	GDC_BOVIN	O01888 bos tauris
32	296.5	19.1	702	CMC1_CAEL	O21153 caenorhabdi
33	296	19.1	588	CMC2_CAEL	O20799 caenorhabdi

ALIGNMENTS

RESULT 1	ADP1_HUMAN	STANDARD:	PRT:	298 AA.
AC	P12235;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	ADP, ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (adenine nucleotide translocator 1) (ANT 1).			
GN	SLC25A4 OR ANT1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid:9606;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-89236396; PubMed-2541251;			
RA	Cozens A.L., Runswick M.J., Walker J.E.;			
RT	"DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.";			
RL	J. Mol. Biol. 206:261-280(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-89340499; PubMed-2547778;			
RA	Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.;			
RT	"A human muscle adenine nucleotide translocator gene has four exons, and is located on chromosome 4, and is differentially expressed.";			
RL	J. Biol. Chem. 264:13998-14004(1989).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-88041149; PubMed-2823266;			
RA	Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;			
RT	"cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader peptide, divergence from a fibroblast translocator cDNA, and coevolution with mitochondrial DNA genes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-Eye;			
RA	Strausberg R.;			
RT	Submitted (May-2001) to the EMBL/Genbank/DBJ databases.			
RL	[5]			
RP	SEQUENCE OF 1-37 FROM N.A.			
RX	TISSUE-Liver;			
RA	MEDLINE-88124845; PubMed-2829183;			
RT	Houdsworth J., Attardi G.;			
RL	"Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in adult human liver.";			
RN	Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).			
RP	VARIANTS PRO PRO-114 AND MET-289.			
RX	MEDLINE-20385067; PubMed-10926541;			
RA	Kauonen J., Juselius J.K., Tiranli V., Kytala A., Zeviani M.,			
RT	Comi G.P., Keranen J., Peltonen L., Suomalainen A.;			
RL	"Role of adenine nucleotide translocator 1 in mtDNA maintenance.";			

P16261 ratu mus norv
Q99297 saccharomyc
P16260 homo sapien
Q9150 homo sapien
Q19529 caenorhabdi
Q912d1 homo sapien
Q99244 mus musculi
Q91K4 homo sapien
Q922b2 mus musculi
Q03028 saccharomyc
Q95258 homo sapien
Q9a73 drosophila

RL Science 289:782-785(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant
 CC progressive external ophthalmoplegia with various mitochondrial
 CC DNA deletions (PEO). Patients with PEO have mitochondrial
 CC myopathy, progressive external ophthalmoplegia, and other
 CC abnormalities associated with multiple different deletions of
 CC mitochondrial DNA.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J02966; AAA61223.1; -;
 DR EMBL: J03593; AAA36751.1; -;
 DR EMBL: J04982; AAA51736.1; -;
 DR EMBL: BC008664; AAH08664.1; -;
 DR PIR: A28116; A28116.
 DR PIR: A39891; A39891.
 DR PIR: S03893; S03893.
 DR PIR: A44778; A44778.
 DR Genew; HGNC:10990; SLC25A4.
 DR MIM; 103220; -;
 DR MIM; 157640; -;
 DR InterPro: IPR002067; Mito_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCH_CARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family; Disease mutation.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 FT VARIANT 114 114
 FT VARIANT 289 289
 FT VARIANT /FTId-Var_012111.
 FT VARIANT V -> M (IN PRO).
 FT VARIANT /FTId-Var_012112.
 FT VARIANT G -> A (IN REF. 3).
 FT CONFLICT 147 149 KGA -> RR (IN REF. 3).
 FT CONFLICT 227 227 V -> L (IN REF. 3).
 SQ SEQUENCE 298 AA; 33064 MW; 59F0DFAC4E7CEB8 CRC64;
 Query Match 98.3%; Score 1526.5; DB 1; Length 298;
 Best Local Similarity 98.3%; Pred. No. 2; 3e-132;
 Matches 293; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
 QY 1 MGDAWMSFLDELGAVAASVTAVPIEVEKLLQVQHASKOISAEKQKGIIDCVYR 60
 DB 1 MGDHANSFLDELGAAGAAVSKTAAPRIEYKLLQVQHASKOISAEKQKGIIDCVYR 60
 QY 1 PKEGGLSEWRGNLANVIRYPTQALNFAFKDXYKQLFLGCVDRHRQFWRYFAGNLASG 120
 DB 1 PKEGGLSEWRGNLANVIRYPTQALNFAFKDXYKQLFLGCVDRHRQFWRYFAGNLASG 120
 QY 121 GAAGATSLCEVYPLDFAFRLADYGR-RAQREHGLGDCIIRKFSKDGRLGYQGFNV 179
 DB 121 GAAGATSLCEVYPLDFAFRLADYGR-RAQREHGLGDCIIRKFSKDGRLGYQGFNV 179

DB 121 GAAGATSLCEVYPLDFAFRLADYGRGAQAREFHGLGDCIIRKFSKDGRLGYQGFNV 180
 QY 180 VQGIITRYAAAFVGYDTAKGMLPDPKRVNHFVSMIAQSVTAVALSLYFEDYRRMM 239
 DB 181 VQGIITRYAAAFVGYDTAKGMLPDPKRVNHFVSMIAQSVTAVALSLYFEDYRRMM 240
 QY 240 QSGRRGADIMYTGVDWCRKIAKDEGAKAFKKGAMSVNLKMGAFVLYLDEIKKYV 297
 DB 241 QSGRRGADIMYTGVDWCRKIAKDEGAKAFKKGAMSVNLKMGAFVLYLDEIKKYV 298
 RESULT 2
 ADT1_RAT
 ID ADT1_RAT STANDARD; PRT; 298 AA.
 AC Q05962;
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 40, Last annotation update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
 DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 GN SLC25A4 OR ANT1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shinozaki Y., Kamida M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RT encoding rat mitochondrial adenine nucleotide translocator.";
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
 CC EXTENT, IN BRAIN AND KIDNEY.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X61667; CAA43842.1; -;
 DR EMBL: D12770; BAA02237.1; -;
 DR InterPro: IPR002067; Mito_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCH_CARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32989 MW; 66704FF78C6BC320 CRC64;
 Query Match 94.4%; Score 1466.5; DB 1; Length 298;
 Best Local Similarity 94.3%; Pred. No. 7e-127;

Matches 281: Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDAHMSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASKQISAEKQYKGIIDCVYR 60
 DB 1 MGDAHMSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASKQISAEKQYKGIIDCVYR 60

QY 61 IPKEGFLSFWRGNLANIYRFFPTQALNFAFKDKYKQFLGVDNRHKQFWRFFAGNLASG 120
 DB 61 IPKEGFLSFWRGNLANIYRFFPTQALNFAFKDKYKQFLGVDNRHKQFWRFFAGNLASG 120

QY 121 GAAGATSLCFYVPLDFATRLAADVGR-RAOREPHGLDCKIKFKSDGLKGLYOGFNV 179
 DB 121 GAAGATSLCFYVPLDFATRLAADVGR-RAOREPHGLDCKIKFKSDGLKGLYOGFNV 179

QY 121 GAAGATSLCFYVPLDFATRLAADVGR-RAOREPHGLDCKIKFKSDGLKGLYOGFNV 179
 DB 121 GAAGATSLCFYVPLDFATRLAADVGR-RAOREPHGLDCKIKFKSDGLKGLYOGFNV 179

QY 180 VOGIIYRAAFGYVDYAKGMLPDPKNVHIFVSMIAQSVTAAGLSYPTDYVRRMM 239
 DB 180 VOGIIYRAAFGYVDYAKGMLPDPKNVHIFVSMIAQSVTAAGLSYPTDYVRRMM 239

QY 240 QSGRKGADIMYTGTCWRKIAKDEGAKAFKAGMSNVLRMGAFVLYVDEIKKYV 297
 DB 240 QSGRKGADIMYTGTCWRKIAKDEGAKAFKAGMSNVLRMGAFVLYVDEIKKYV 297

QY 241 QSGRKGADIMYTGTCWRKIAKDEGAKAFKAGMSNVLRMGAFVLYVDEIKKYV 298
 DB 241 QSGRKGADIMYTGTCWRKIAKDEGAKAFKAGMSNVLRMGAFVLYVDEIKKYV 298

RESULT 3

ADTL_MOUSE
 ID ADTL_MOUSE STANDARD: PRT: 298 AA.

AC PA8962: 062164;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (MANC1).
 GN SIC25A4 OR ANTI OR ANCI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=97059403; PubMed=8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse homologs."
 RT Mamm. Genome 7:25-30(1996).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Muscle;
 RA Laplace C., Costet P.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: U27315; AAC52837.1; -;
 DR EMBL: X74510; CAAS2616.1; -;
 DR EMBL: AF240002; AAF64470.1; -;
 DR EMBL: BC003791; AAH03791.1; -;
 DR EMBL: BC026925; AAH26925.1; -;
 DR MGD: MGI:1353495; SIC25a4.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3
 DR PRINTS: PR00826; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 136 136 F->L (IN REF. 1).
 SO SEQUENCE 298 AA; 32904 MW; 3A849FEB0981462 CRC64;

Query Match 94.2%; Score 1463.5; DB 1; Length 298;
 Best Local Similarity 94.0%; Pred. No. 1.3e-126;
 Matches 280: Conservative 10; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDAHMSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASKQISAEKQYKGIIDCVYR 60
 DB 1 MGDAHMSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASKQISAEKQYKGIIDCVYR 60

QY 61 IPKEGFLSFWRGNLANIYRFFPTQALNFAFKDKYKQFLGVDNRHKQFWRFFAGNLASG 120
 DB 61 IPKEGFLSFWRGNLANIYRFFPTQALNFAFKDKYKQFLGVDNRHKQFWRFFAGNLASG 120

QY 121 GAAGATSLCFYVPLDFATRLAADVGR-RAOREPHGLDCKIKFKSDGLKGLYOGFNV 179
 DB 121 GAAGATSLCFYVPLDFATRLAADVGR-RAOREPHGLDCKIKFKSDGLKGLYOGFNV 179

QY 121 GAAGATSLCFYVPLDFATRLAADVGR-RAOREPHGLDCKIKFKSDGLKGLYOGFNV 179
 DB 121 GAAGATSLCFYVPLDFATRLAADVGR-RAOREPHGLDCKIKFKSDGLKGLYOGFNV 179

QY 180 VOGIIYRAAFGYVDYAKGMLPDPKNVHIFVSMIAQSVTAAGLSYPTDYVRRMM 239
 DB 180 VOGIIYRAAFGYVDYAKGMLPDPKNVHIFVSMIAQSVTAAGLSYPTDYVRRMM 239

QY 240 QSGRKGADIMYTGTCWRKIAKDEGAKAFKAGMSNVLRMGAFVLYVDEIKKYV 297
 DB 240 QSGRKGADIMYTGTCWRKIAKDEGAKAFKAGMSNVLRMGAFVLYVDEIKKYV 297

QY 241 QSGRKGADIMYTGTCWRKIAKDEGAKAFKAGMSNVLRMGAFVLYVDEIKKYV 298
 DB 241 QSGRKGADIMYTGTCWRKIAKDEGAKAFKAGMSNVLRMGAFVLYVDEIKKYV 298

RESULT 4

ADTL_BOVIN
 ID ADTL_BOVIN STANDARD: PRT: 297 AA.

AC P02722;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP carrier protein, heart isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 GN SIC25A4 OR ANTI.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovidae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89229093; PubMed=2540808;
 RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;

```

RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues."
RL Biochemistry 28:866-873(1989).
RN [2]
RP SEQUENCE.
RX MEDLINE=82188267; PubMed=7076130;
RA Aquila H., Misra D., Eulitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
RT mitochondria."
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
RN [3]
RP SEQUENCE OF 207-297 FROM N.A.
RX MEDLINE=86295775; PubMed=3017341;
RA Rasmussen U.B., Wohlrab H.;
RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
RT an unusually short 3'-noncoding sequence."
RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M13783; AAA30363.1; -.
DR EMBL: M24102; AAA30768.1; -.
DR PIR: A03181; XMO.
DR PIR: A24822; A24822.
DR PIR: A43646; A43646.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mitochl_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family; Methylation.
FT INIT MET 0 0
FT MOD_RES 1 1 BLOCKED.
FT MOD_RES 51 51 METHYLATION (POTENTIAL).
FT TRANSMEM 11 28 1 (POTENTIAL).
FT TRANSMEM 72 90 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 175 194 4 (POTENTIAL).
FT TRANSMEM 213 230 5 (POTENTIAL).
FT TRANSMEM 272 290 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40AEB48 CRC64;

Query Match 93.6%; Score 1453.5; DB 1; Length 297;
Best Local Similarity 94.6%; Pred. NO. 11e-125;
Matches 280; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

```

```

DB 122 AGATSLCFYPLDFAFRTLAADVGAAGAREFTGLGNCITKIFKSDGLRGLYGFNVSVQ 181
OY 182 GIITRAAFYGYDPAKGLPDPKVNHTFVSMIAQSYTAVALGSLYFEDYRRMMQMS 241
DB 182 GIITRAAFYGYDPAKGLPDPKVNHTFVSMIAQSYTAVALGSLYFEDYRRMMQMS 241
OY 242 GRKADIMYTGTVDCWRKIADKAGAKAFKGMNSVLRGMGAFVLYLDEIKRYV 297
DB 242 GRKADIMYTGTVDCWRKIADKAGAKAFKGMNSVLRGMGAFVLYLDEIKRYV 297

RESULT 5
ADP2_MOUSE STANDARD: PRT; 298 AA.
AC P51881; 061311;
DT 01-OCT-1996 (Rel. 34, created)
DT 01-OCT-1996 (Rel. 34, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
RT homologs."
RL Mamm. Genome 7:25-30(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Sheldon J.G.;
RL Thesis (1995), University of Cambridge, U.K.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA Costet P., Laplace C.;
RL Submitted (Feb-1993) to the EMBL/GenBank/DBJ databases.
RN [4]
RP REVISIONS.
RA Laplace C.;
RL Submitted (Feb-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=20432087; PubMed=10974536;
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide
RT translocase 1 and 2 genes."
RL Gene 254:57-66(2000).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U27316; AAC52838.1; -.
DR EMBL: U10404; AAA19009.1; -.
DR EMBL: X70847; CAA50196.1; -.

```



```

DR EMBL: AF240003; AAF64471.1; -
DR MGD: MGI:1353496; SLOC25a5.
DR InterPro: IPR002067; Mito_carrler.
DR InterPro: IPR001993; Mitoch_carrler.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER.
DR Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32931 MW; 0798E04B987EFE20 CRC64;

Query Match 90.7%; Score 1408.5; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 1.4e-121;
Matches 266; Conservative 17; Mismatches 13; Indels 1; Gaps 1;

OY 1 MGDHANSFLKDFLAGVAAVASTAVAPIERVKLLQVGHASQISAEKQYGIIDCVVR 60
DB 1 MTDAAVSFAKDFLAGGVAAVASTAVAPIERVKLLQVGHASQISAEKQYGIIDCVVR 60
OY 61 IPKEQGLSFWKGNLNVIRYPTQALNFAFKDKYKQLFGVDRKQFWRYPAGNLASG 120
DB 61 IPKEQGLSFWKGNLNVIRYPTQALNFAFKDKYKQLFGVDRKQFWRYPAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARFLAADVGR-AQREFHGLGDCIIRKFSKDLGLGYGFNVS 179
DB 121 GAAGATSLCFVYPLDFARFLAADVGR-AQREFHGLGDCIIRKFSKDLGLGYGFNVS 179
OY 121 GAAGATSLCFVYPLDFARFLAADVGR-AQREFHGLGDCIIRKFSKDLGLGYGFNVS 180
DB 121 GAAGATSLCFVYPLDFARFLAADVGR-AQREFHGLGDCIIRKFSKDLGLGYGFNVS 180
OY 180 VGGIITRYRAAYGVYDTAGMLPDPKNVHIFVSWMTAOSTAVAGLSTPFDVRRRMM 239
DB 180 VGGIITRYRAAYGVYDTAGMLPDPKNVHIFVSWMTAOSTAVAGLSTPFDVRRRMM 240
OY 240 QSGRKADIMYGTVDCKMRKIADEGAKAFKFGAMSNVLRMGAGVLLVLYDEIKKY 296
DB 240 QSGRKADIMYGTVDCKMRKIADEGAKAFKFGAMSNVLRMGAGVLLVLYDEIKKY 297

RESULT 6
ADT2_RAT STANDARD; PRT; 298 AA.
AC 009073;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shiohara Y., Kamida M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone
encoding rat mitochondrial adenine nucleotide translocator.";
RL Biochim. Biophys. Acta 1152:192-196(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND

```

```

CC CC SKELETAL MUSCLE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: D12771; BAA02238.1; -
DR InterPro: IPR002067; Mito_carrler.
DR InterPro: IPR001993; Mitoch_carrler.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER.
DR Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987EFE35 CRC64;

Query Match 90.6%; Score 1407.5; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 1.7e-121;
Matches 266; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

OY 1 MGDHANSFLKDFLAGVAAVASTAVAPIERVKLLQVGHASQISAEKQYGIIDCVVR 60
DB 1 MTDAAVSFAKDFLAGGVAAVASTAVAPIERVKLLQVGHASQISAEKQYGIIDCVVR 60
OY 61 IPKEQGLSFWKGNLNVIRYPTQALNFAFKDKYKQLFGVDRKQFWRYPAGNLASG 120
DB 61 IPKEQGLSFWKGNLNVIRYPTQALNFAFKDKYKQLFGVDRKQFWRYPAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARFLAADVGR-AQREFHGLGDCIIRKFSKDLGLGYGFNVS 179
DB 121 GAAGATSLCFVYPLDFARFLAADVGR-AQREFHGLGDCIIRKFSKDLGLGYGFNVS 180
OY 121 GAAGATSLCFVYPLDFARFLAADVGR-AQREFHGLGDCIIRKFSKDLGLGYGFNVS 179
DB 121 GAAGATSLCFVYPLDFARFLAADVGR-AQREFHGLGDCIIRKFSKDLGLGYGFNVS 180
OY 180 VGGIITRYRAAYGVYDTAGMLPDPKNVHIFVSWMTAOSTAVAGLSTPFDVRRRMM 239
DB 180 VGGIITRYRAAYGVYDTAGMLPDPKNVHIFVSWMTAOSTAVAGLSTPFDVRRRMM 240
OY 240 QSGRKADIMYGTVDCKMRKIADEGAKAFKFGAMSNVLRMGAGVLLVLYDEIKKY 296
DB 240 QSGRKADIMYGTVDCKMRKIADEGAKAFKFGAMSNVLRMGAGVLLVLYDEIKKY 297

RESULT 7
ADT2_HUMAN STANDARD; PRT; 298 AA.
AC P05141; O43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;

```

RX MEDLINE=90375457; PubMed=2168878;
 RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurtzel J.;
 RT "The human fibroblast adenine nucleotide translocator gene. Molecular
 RT cloning and sequence.";
 RL J. Biol. Chem. 265:16060-16063(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87166056; PubMed=3031073;
 RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
 RA Baserga R.;
 RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
 RT growth-regulated.";
 RL J. Biol. Chem. 262:4355-4358(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Chen C.N., Su Y., Bayhayan P., Siruno A., Nagareja R.,
 RA Mazzarella R.A., Schlessinger D., Chen E.Y.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Becker M., Graves T., Ozersky P.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 47-298 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Attardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 RT level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M57424; AAA51737.1; -;
 DR EMBL: J02683; AAA35579.1; -;
 DR EMBL: L78810; AAB39266.1; -;
 DR EMBL: AC004000; AAB96347.1; -;
 DR EMBL: J03591; AAA36749.1; -;
 DR PIR: A29132; A29132.
 DR PIR: C28116; C28116.
 DR Genew; HGNC:10991; SLC25A5.
 DR MIM; 300150; -;
 DR InterPro; IPR002067; Mit_carrier.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 4 (POTENTIAL).
 FT TRANSMEM 273 291 5 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 6 6 V -> L (IN REF. 2).
 FT CONFLICT 66 66 G -> E (IN REF. 2).

FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
 FT CONFLICT 162 162 V -> G (IN REF. 5).
 SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;
 Query Match 90.1%; Score 1398.5; DB 1; Length 298;
 Best Local Similarity 88.9%; Pred. No. 1,2e-120;
 Matches 264; Conservative 17; Mismatches 15; Indels 1; Gaps 1;
 QY 1 MGDHMSFLDPLAGAAVAASKTAAPVIRVLLLOVHASQIOISAEKYGKIIICVVR 60
 DB 1 MTDAAVSFAKDFLAGVAAIAISKTAAPVIRVLLLOVHASQIOISAEKYGKIIICVVR 60
 QY 61 IPKEGFLSFWRGNLANVIRYFPPTQALNFAFKDKYKOLFGLGVDRHKEFRYFAGNLAAG 120
 DB 61 IPKEGVLSTWRGNLANVIRYFPPTQALNFAFKDKYKOLFGLGVDRHKEFRYFAGNLAAG 120
 QY 121 GAAGATSLCEVYPLDFARTLADVCGRR-AQREFHGLGDCIIFKSDGLRGLYQGFNV 179
 DB 121 GAAGATSLCEVYPLDFARTLADVCGRR-AQREFHGLGDCIIFKSDGLRGLYQGFNV 180
 QY 180 VGGITIRAAVPGYDFAKGMIDDPKRVHIFVSMITQSVTAAGILSTYFEDVRRRMM 239
 DB 181 VGGITIRAAVPGYDFAKGMIDDPKRVHIFVSMITQSVTAAGILSTYFEDVRRRMM 240
 QY 240 QSGRKGADIMYGTGDCWRKRIANDGAKAFKGAWSNVLKMGAFVLYLDEIKRY 296
 DB 241 QSGRKGADIMYGTGDCWRKRIANDGAKAFKGAWSNVLKMGAFVLYLDEIKRY 297
 RESULT 8
 ADT3_HUMAN STANDARD; PRT; 298 AA.
 ID ADT3_HUMAN
 AC P12336; O96C49;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
 GN (Adenine nucleotide translocator 3) (ANT 3).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89236396; PubMed=2541251;
 RA Cozens A.L., Runswick M.J., Walker J.E.;
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial
 RT ADP/ATP translocase.";
 RL J. Mol. Biol. 206:261-280(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
 RA Margolin J.F.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Cervix, Eye, and Lung;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 36-298 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Attardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 RT level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.

```
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J03592; AAA36750.1; -
CC EMBL: AY007135; AAG01998.1; -
CC EMBL: BC007295; AAH07295.1; -
CC EMBL: BC007850; AAH07850.1; -
CC EMBL: BC008737; AAH08737.1; -
CC EMBL: BC008935; AAH08935.1; -
CC EMBL: BC014775; AAH14775.1; -
CC PIR: S03894; S03894.
CC PIR: B28116; B28116.
CC Genew: HGNC:10992; SLC25A6.
CC MIM: 403001; -
CC MIM: 300151; -
CC InterPro: IPR002067; Mit_carrier.
CC InterPro: IPR001993; Mitoch_carrier.
CC Pfam: PF00153; mitoc_carr; 3.
CC PRINTS: PR00926; MITOCARRIER.
CC PROSITE: PS00215; MITOCH_CARRIER; 3.
CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
CC Multigene family.
CC FT TRANSMEM 12 29 1 (POTENTIAL).
CC FT TRANSMEM 73 91 2 (POTENTIAL).
CC FT TRANSMEM 117 134 3 (POTENTIAL).
CC FT TRANSMEM 176 195 4 (POTENTIAL).
CC FT TRANSMEM 214 231 5 (POTENTIAL).
CC FT TRANSMEM 273 291 6 (POTENTIAL).
CC FT REPEAT 1 100 1.
CC FT REPEAT 101 208 2.
CC FT REPEAT 209 298 3.
CC FT CONFLICT 105 108 3.
CC FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
CC FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
CC FT SEQUENCE 298 AA; 32866 MW; 18534E9F0E49672F CRC64;

Query Match 89.2%; Score 1385.5; DB 1; Length 298;
Best Local Similarity 87.2%; Pred. No. 1.8e-119;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHANSFLKDLFLAGAAVAAVSKTAAVPIERVKLLQVQHASQISAEKQYKGIIDCVR 60
   1 MTDQALSFADKFLAGIAAIAISTAVAPIERVKLLQVQHASQISAEKQYKGIIDCVR 60
DB 1 MTDQALSFADKFLAGIAAIAISTAVAPIERVKLLQVQHASQISAEKQYKGIIDCVR 60

OY 61 IPKEGFLSFWRGNLANVIRFPPTQALNFAFKDKYKQLFLGVDNRHQRKQFRYFAGNLSG 120
   61 IPKEGFLSFWRGNLANVIRFPPTQALNFAFKDKYKQLFLGVDNRHQRKQFRYFAGNLSG 120
DB 61 IPKEGFLSFWRGNLANVIRFPPTQALNFAFKDKYKQLFLGVDNRHQRKQFRYFAGNLSG 120

OY 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREFHGLGDCIIFKSDGLRGLYOGFNVS 179
   121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREFHGLGDCIIFKSDGLRGLYOGFNVS 179
DB 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREFHGLGDCIIFKSDGLRGLYOGFNVS 179

OY 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREFHGLGDCIIFKSDGLRGLYOGFNVS 179
   121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREFHGLGDCIIFKSDGLRGLYOGFNVS 179
DB 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREFHGLGDCIIFKSDGLRGLYOGFNVS 179

OY 180 VQGIITIRAAVFGVYDTAKMLDPKKNVHIFVSMMLAQSTAAVAGLLSYDFDVRRRMM 239
   180 VQGIITIRAAVFGVYDTAKMLDPKKNVHIFVSMMLAQSTAAVAGLLSYDFDVRRRMM 239
DB 180 VQGIITIRAAVFGVYDTAKMLDPKKNVHIFVSMMLAQSTAAVAGLLSYDFDVRRRMM 239

OY 181 VQGIITIRAAVFGVYDTAKMLDPKKNVHIFVSMMLAQSTAAVAGLLSYDFDVRRRMM 240
   181 VQGIITIRAAVFGVYDTAKMLDPKKNVHIFVSMMLAQSTAAVAGLLSYDFDVRRRMM 240
DB 181 VQGIITIRAAVFGVYDTAKMLDPKKNVHIFVSMMLAQSTAAVAGLLSYDFDVRRRMM 240

OY 240 QSRKAGADIMYGTVDCKRIANDEGAFAFKGAMSVNLKMGAGFVLYLDEIKKYV 297
   240 QSRKAGADIMYGTVDCKRIANDEGAFAFKGAMSVNLKMGAGFVLYLDEIKKYV 297
DB 240 QSRKAGADIMYGTVDCKRIANDEGAFAFKGAMSVNLKMGAGFVLYLDEIKKYV 297

OY 241 QSRKAGADIMYGTVDCKRIANDEGAFAFKGAMSVNLKMGAGFVLYLDEIKKYV 298
   241 QSRKAGADIMYGTVDCKRIANDEGAFAFKGAMSVNLKMGAGFVLYLDEIKKYV 298
DB 241 QSRKAGADIMYGTVDCKRIANDEGAFAFKGAMSVNLKMGAGFVLYLDEIKKYV 298

RESULT 9
ADT3_BOVIN STANDARD: PRT; 298 AA.
ID ADT3_BOVIN AC P32007;
DT 01-JUL-1993 (Rel. 26, Created)
```

```
DT 01-JUL-1993 (Rel. 26, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE ADP ATP carrier protein, Isoform 72 (ADP/ATP translocase 3) (Adenine
DE nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
DE Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
ON (1)
RX SEQUENCE FROM N.A.
RX MEDLINE=89229093; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues.
RL Biochemistry 28:866-873(1989).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M24103; AAA30769.1; -
CC PIR: B43646; B43646.
CC InterPro: IPR002067; Mit_carrier.
CC InterPro: IPR001993; Mitoch_carrier.
CC Pfam: PF00153; mitoc_carr; 3.
CC PRINTS: PR00926; MITOCARRIER.
CC PROSITE: PS00215; MITOCH_CARRIER; 3.
CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
CC Multigene family.
CC FT TRANSMEM 12 29 1 (POTENTIAL).
CC FT TRANSMEM 73 91 2 (POTENTIAL).
CC FT TRANSMEM 117 134 3 (POTENTIAL).
CC FT TRANSMEM 176 195 4 (POTENTIAL).
CC FT TRANSMEM 214 231 5 (POTENTIAL).
CC FT TRANSMEM 273 291 6 (POTENTIAL).
CC FT REPEAT 1 111 1.
CC FT REPEAT 112 208 2.
CC FT REPEAT 209 298 3.
CC FT SEQUENCE 298 AA; 32877 MW; 1C34E7F6DEDE4061 CRC64;

Query Match 88.9%; Score 1380.5; DB 1; Length 298;
Best Local Similarity 86.9%; Pred. No. 5.1e-119;
Matches 259; Conservative 21; Mismatches 17; Indels 1; Gaps 1;

OY 1 MGDHANSFLKDLFLAGAAVAAVSKTAAVPIERVKLLQVQHASQISAEKQYKGIIDCVR 60
   1 MTDQALSFADKFLAGIAAIAISTAVAPIERVKLLQVQHASQISAEKQYKGIIDCVR 60
DB 1 MTDQALSFADKFLAGIAAIAISTAVAPIERVKLLQVQHASQISAEKQYKGIIDCVR 60

OY 61 IPKEGFLSFWRGNLANVIRFPPTQALNFAFKDKYKQLFLGVDNRHQRKQFRYFAGNLSG 120
   61 IPKEGFLSFWRGNLANVIRFPPTQALNFAFKDKYKQLFLGVDNRHQRKQFRYFAGNLSG 120
DB 61 IPKEGFLSFWRGNLANVIRFPPTQALNFAFKDKYKQLFLGVDNRHQRKQFRYFAGNLSG 120

OY 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREFHGLGDCIIFKSDGLRGLYOGFNVS 179
   121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREFHGLGDCIIFKSDGLRGLYOGFNVS 179
DB 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREFHGLGDCIIFKSDGLRGLYOGFNVS 179

OY 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREFHGLGDCIIFKSDGLRGLYOGFNVS 179
   121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREFHGLGDCIIFKSDGLRGLYOGFNVS 179
DB 121 GAAGATSLCFVYPLDFAFRTLAADVGR-AQREFHGLGDCIIFKSDGLRGLYOGFNVS 179

OY 180 VQGIITIRAAVFGVYDTAKMLDPKKNVHIFVSMMLAQSTAAVAGLLSYDFDVRRRMM 239
   180 VQGIITIRAAVFGVYDTAKMLDPKKNVHIFVSMMLAQSTAAVAGLLSYDFDVRRRMM 239
DB 180 VQGIITIRAAVFGVYDTAKMLDPKKNVHIFVSMMLAQSTAAVAGLLSYDFDVRRRMM 239

OY 181 VQGIITIRAAVFGVYDTAKMLDPKKNVHIFVSMMLAQSTAAVAGLLSYDFDVRRRMM 240
   181 VQGIITIRAAVFGVYDTAKMLDPKKNVHIFVSMMLAQSTAAVAGLLSYDFDVRRRMM 240
DB 181 VQGIITIRAAVFGVYDTAKMLDPKKNVHIFVSMMLAQSTAAVAGLLSYDFDVRRRMM 240
```

QY 240 OSGRKADIMYGTGTCVDCWRKIADKAGAFKFGAMSNVLRMGSAFVLVLYDEIKKYV 297
 ID 241 OSGRKADIMYGTGTCVDCWRKIADKAGAFKFGAMSNVLRMGSAFVLVLYDEIKKYV 298
 Db 241 OSGRKADIMYGTGTCVDCWRKIADKAGAFKFGAMSNVLRMGSAFVLVLYDEIKKYV 298
 RESULT 10
 ADT_DROME STANDARD; PRT; 297 AA.
 AC 026365; 026254; P91614; G9V270;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP/ATP carrier protein (ADP/ATP translocase) (adenine nucleotide
 translocator) (ANT) (Stress sensitive B protein).
 GN SESB OR A/A-T OR CG16944.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92389367; PubMed=1387687;
 RA Louvi A., Tsiftlidou S.G.;
 RT "A cDNA clone encoding the ADP/ATP translocase of Drosophila
 RT melanogaster shows a high degree of similarity with the mammalian
 RT ADP/ATP translocases.";
 RL J. Mol. Evol. 35:44-50(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94350065; PubMed=7520869;
 RA Hutter P., Karch F.;
 RT "Molecular analysis of a candidate gene for the reproductive
 RT isolation between sibling species of Drosophila.";
 RL Experientia 50:749-762(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R;
 RA Zhang Y.Q., Davis A.W., Roote J., Hermann S., Ashburner M.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintinas S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Paulis B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodier A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaiswal M., Kalish J., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson A.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson S.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Syriakas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Massaman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane (By similarity).
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; S43651; AAB2314.1; -;
 DR EMBL; S71762; AAB31734.3; -;
 DR EMBL; Y10618; CAA71628.1; -;
 DR EMBL; AE003484; AAF47957.1; -;
 DR FlyBase; Fggn0003360; sesb.
 DR InterPro; IPR002067; MLC_carrier.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00153; mito_carrier_3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER_3.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 14 31 1 (POTENTIAL).
 FT TRANSMEM 75 93 2 (POTENTIAL).
 FT TRANSMEM 119 136 3 (POTENTIAL).
 FT TRANSMEM 177 196 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 272 290 6 (POTENTIAL).
 FT TRANSMEM 18 19 QV -> GI (IN REF. 3 AND 4).
 FT CONFLICT 81 81 I -> Y (IN REF. 1).
 FT CONFLICT 200 200 R -> RG (IN REF. 3 AND 4).
 FT CONFLICT 266 266 G -> A (IN REF. 2).
 FT CONFLICT 267 268 PC -> TGA (IN REF. 3 AND 4).
 FT CONFLICT 268 268 C -> S (IN REF. 1).
 SQ SEQUENCE .297 AA; 32880 MW; AA639439968F9750 CRC64;
 Query Match 78.0%; Score 1211; DB 1; Length 297;
 Best Local Similarity 79.4%; Pred. No. 1,6e-103;
 Matches 231; Conservative 25; Mismatches 33; Indels 2; Gaps 2;
 QY 5 AMSELDKFLAGAAVAASKTAVADIERYKLLQVQHASKQDISAKQYKGIIDCVRIKPE 64
 Db 7 AVGVCFDPAAGQVSAASKTAVADIERYKLLQVQHASKQDISAKQYKGIIDCVRIKPE 66
 QY 65 OGFLSPFRGNLANIYRFFPTQALNFARFKDKKQQLFGLGVYDHNKQFMYRFGNLSAGGA 124
 Db 67 OGFSSEFWGNLANIYRFFPTQALNFARFKDKKQQLFGLGVYDHNKQFMYRFGNLSAGGA 126
 QY 125 ATSLCFVYPLDFAFTRTLAADVGRRAOREFHLGDCIIRIKFSDGLRGLYGFNFVYOGII 184
 Db 127 ATSLCFVYPLDFAFTRTLAADVGRRAOREFHLGDCIIRIKFSDGLRGLYGFNFVYOGII 186
 QY 185 TYRAVFGVYDTAKGMLDPKRNVIHFWSMIAQSVTAAGLSYPTDTRRRMMQSGRK 244
 Db 187 TYRAVFGVYDTAKGMLDPKRNVIHFWSMIAQSVTAAGLSYPTDTRRRMMQSGRK 245
 QY 245 GADIMYGTGTCVDCWRKIADKAGAFKFGAMSNVLRMGSAFVLVLYDEIKK 295
 Db 246 ATEVIYKNTLHCWATIAKQEG-PCFFGAGAFSNILRGTCGAFVLVLYDEIKK 295


```

Db 159 AGLLLVPLDFAFRTLRLAADVGSKSEFGLDCLSKVYKRGPMALYGFVSGIIT 218
QY 185 IYSAAYGVYDTAKML-PDPKNVHIFVSMIAOSTAVAGLSYDPDVRRRMMQSGR 243
Db 219 VYRGATFGLDVTAKGLFKEKRTANFPAKVAVAVATAGAGVLSYDPDVRRRMMQSG-- 276
QY 244 KGADIMYTGTVDCMRKIADKDEGAKAFKAGMSVNLKMGAFVLYLDEIKKYV 297
Db 277 -GGERQYNGTIDCMRKRYAOGEGMKAFKAGMSVNLGAGGAFVLYLDEIKKFI 329

RESULT 13
ADT_CHLRE STANDARD; PRT; 308 AA.
AC P27080;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (adenine nucleotide translocator) (ANT).
GN ABT.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=FUDA4-R2;
RX MEDLINE=93204887; PubMed=8455552;
RA Sharpe J.A., Day A.;
RT "Structure, evolution and expression of the mitochondrial ADP/ATP mol. Genet. 237:134-144(1993).";
RL 1.
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.ch/announce/ or send an email to license@isb-sib.ch).
CC
CC EMBL: X65194; CAA46311.1; -
CC PIR: S30259; S30259.
CC InterPro: IPR002067; Mlt_carrier.
CC InterPro: IPR001993; Mitoch_carrier.
CC Pfam: PF00153; Mito_carr1.3.
CC PRINTS: PR00926; MITOCH_CARRIER.
CC PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 74 92 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 178 197 4 (POTENTIAL).
FT TRANSMEM 217 234 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
SQ SEQUENCE 308 AA; 33528 MW; D477CF0E72B7A53F CRC64;

Query Match 49.6%; Score 770.5; DB 1; Length 308;
Best Local Similarity 52.6%; Pred. No. 3,4e-63;
Matches 159; Conservative 49; Mismatches 77; Indels 17; Gaps 6;
QY 7 SFLKDLFAGVAANAIVSTAVPIERVYLLQVQ-HASKQISAQKQYGIIDCVIRIKEQ 65
Db 7 NFWVDLFGGLSAVSKTAAPIERVYLLQVQDEMIKQGLASPKYIGECFVIRVEE 66

```

```

QY 66 GFLSFWRGNLANIVRYEPQALNFAFKDKYKQLELGVDRHKOFWRYFAGNLASGAGA 125
Db 67 GFGLSLRGNTANIVRYEPQALNFAFKDKRNF--GFNKDKRYKMFPGNNASGAGA 124
QY 126 TSLCEVYPLDFARTRLAADVGR---ADREFGLDCCIIFKFSGLRGLYGFVNSVQ 181
Db 125 VSLSPYSLDVFARTRLANDAKSAKKGCGDQFNGLDVYVRKTIASDGIAGLYRGNISCV 184
QY 182 GIIYFAAAYGVYDTAKG-MLPDPKNVHIFVSMIAOSTAVAGLSYDPDVRRRMMQ 240
Db 185 GIIVYRGLIFGMYDSLKPVVGLVGLANNPLAFLGLMGITIGAGLSYPLDITRRMMNT 244
QY 241 SGRKGADIMYTGTVDCMRKIADKDEGAKAFKAGMSVNLKMGAFVLYLDEI-----K 294
Db 245 S---GSAVKYNSHFQGEIVKNEGKSLFKGAGANILRVAGVLAGVLDQVILLCK 301
QY 295 KY 296
Db 302 KY 303

RESULT 14
ADT_MAIZE STANDARD; PRT; 387 AA.
AC P04709;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein 1, mitochondrial precursor (ADP/ATP translocase 1) (adenine nucleotide translocator 1) (ANT 1).
GN ANTI OR ANT-G1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=MUTIND-FR7205034;
RX MEDLINE=91322533; PubMed=1863785;
RA Wlanning B.M., Day C.D., Sarah C.J., Leaver C.J.;
RT "Nucleotide sequence of two cDNAs encoding the adenine nucleotide translocator from Zea mays L.";
RL Plant Mol. Biol. 17:305-307(1991).
RN (2)
RP SEQUENCE OF 59-387 FROM N.A.
RC STRAIN-CV. B37N;
RX MEDLINE=8938399; PubMed=2547608;
RA Leaver C.J., Bathgate B., Baker A.;
RT "Two genes encode the adenine nucleotide translocator of maize mitochondria. Isolation, characterisation and expression of the structural genes";
RL Eur. J. Biochem. 183:303-310(1989).
RN (3)
RP SEQUENCE OF 70-387 FROM N.A.
RX MEDLINE=85297781; PubMed=2994015;
RA Baker A., Leaver C.J.;
RT "Isolation and sequence analysis of a cDNA encoding the ATP/ADP translocator of Zea mays L.";
RL Nucleic Acids Res. 13:5857-5867(1985).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

```


modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: X57556; CAA40781.1; -
 CC EMBL: X15711; CAA3742.1; -
 DR EMBL: X02842; CAA26600.1; -
 DR PIR: A24072; A24072.
 DR PIR: S05199; S05199.
 DR PIR: S14876; S14876.
 DR MaltZDB: 17145; -
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr. 3-
 DR PRINTS: PR00926; MITOCH_CARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 2.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Transil peptide; Multigene family.
 FT TRANSIT 1 77 MITOCHONDRION.
 FT CHAIN 1 77 ADP/ATP CARRIER PROTEIN 1.
 FT TRANSMEM 91 108 1 (POTENTIAL).
 FT TRANSMEM 153 171 2 (POTENTIAL).
 FT TRANSMEM 196 213 3 (POTENTIAL).
 FT TRANSMEM 257 276 4 (POTENTIAL).
 FT TRANSMEM 296 313 5 (POTENTIAL).
 FT TRANSMEM 352 370 6 (POTENTIAL).
 FT TRANSMEM 102 102 K -> E (IN REF. 2).
 FT CONFLICT 154 154 N -> Y (IN REF. 3).
 FT CONFLICT 154 154 K -> Y (IN REF. 3).
 SQ SEQUENCE 387 AA; 42391 MW; DE73B0F478BD57D CRC64;

Query Match 48.7%; Score 756.5; DB 1; Length 387;
 Best Local Similarity 53.8%; Pred. No. 8,4e-62;
 Matches 164; Conservative 41; Mismatches 77; Indels 23; Gaps 7;

OY 7 SELKDLGAVAAVAASKTAPVAPRIEYKLLQVQ-HASKOISAEKQYKGIIDCVRIPIKQ 65
 DB 86 NEMIDFEMMGVSAVAASKTAAPIERVKLLIQNDDEMIKSGRLSEPEYKGIIDCVRIKDE 145
 OY 66 GLTSPFRGLAVVIRFPPQALNFAFKDKYKQLFLGCVRRHKQFMYFPGNLSGGAQA 125
 DB 146 GSSSLRGNTAVVIRFPPQALNFAFKDKYKQLFLGCVRRHKQFMYFPGNLSGGAQA 204
 OY 126 TSLCEVYPPDFAFTRLAADVRR---AOREFHGDCIIRKFSDDLKGLYGFENSVQ 182
 DB 205 SSLFVYSLDYARTRLANAKAKGGEKQFNGLVYKRTLSKDSIAGLRFFNISCVG 264
 OY 183 IITIRAAVGYVDYAK-----GMLPDPKNVHIFVSMIAQSVYAVAGLLSYEDTVRRR 237
 DB 265 IIVYRGLYGLVDSIKPVVLTGNLQD---NFFASFALMLITNGAGLASYPIDTVRRR 320
 OY 238 MMQSGKKGADIMYTGVDCKRIAKDEGAKAPFKGMSNVLRMGAFVLYLDEL----- 293
 DB 321 MMTSGEA---VRYKSLDAFQOLKKEGPKSLFKGAGANILRAIAGVLSGYDQLILE 377
 OY 294 --KKY 296
 DB 378 FGKRY 382

RESULT 15
 ADT_SCHPO
 ID ADT_SCHPO STANDARD: PRT: 322 AA.
 AC 009188:
 DT 01-NOV-1997 (rel. 35, Created)
 DT 01-NOV-1997 (rel. 35, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
 GN ANCI OR SPBC530.10C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.

OY NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=96257204; PubMed=8675018;
 RA Coulin N., Treseguet V., Saux A.L., Languin G.J.M.;
 RT "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation in Saccharomyces cerevisiae.";
 RL Gene 171:113-117(1996).
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Oell C., Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volkhardt G., Aert R., Robben J., Grymonprez B., Welljens I., Wolckhaert G., Aert R., Robben J., Grymonprez B., Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Medler H., Wambut R., Purrelle B., Goffeau A., Cadieu E., Diano S., Gloux S., Leclaire V., Mottier S., Gallberg F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -I- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: Z49974; CAA90275.1; -
 DR EMBL: AL023634; CAA19176.1; -
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr. 3-
 DR PRINTS: PR00926; MITOCH_CARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 2.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 28 48 1 (POTENTIAL).
 FT TRANSMEM 93 111 2 (POTENTIAL).
 FT TRANSMEM 131 151 3 (POTENTIAL).
 FT TRANSMEM 197 217 4 (POTENTIAL).
 FT TRANSMEM 222 242 5 (POTENTIAL).
 FT TRANSMEM 289 309 6 (POTENTIAL).
 SQ SEQUENCE 322 AA; 8AC3D16A40FA4AFC CRC64;

Query Match 48.5%; Score 752.5; DB 1; Length 322;

Best Local Similarity 52.9%, Pred. No. 1,6e-61,
Matches 156; Conservative 51; Mismatches 75; Indels 13; Gaps 6;

```
OY      7 SFLKDFLAGAANAASKTAAVAETEEVKILLLOVONHAKOISAEEK---QYKGIIDCVVRIPK 63  
       : || : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db     26 TEEFFPMFGGVSAASAKTAAPAEIEVKLLIQNQ--DEMIAGRLSHRYKGICECEKPTAA 83  
  
OY     64 EGGSLSPMRGNLANIIRPPOALNFAFKDKKKLYOLELGLVDNHKQFWMYRFGNLSSGA 123  
       :| : : | ||||| ||||| ||||| ||||| ||||| : : : ||||| : : ||||| :  
Db     84 EEGVLSIMRGNAVLRIETPDALNFARKDKFKNKF-GIKKERDGYATWFMGAINLSSGA 142  
  
OY    124 GATSLCFYVPPLDEFARTLAAD---VGRAAROREFHLDSCIIIFEKSDGRGLQGPFNSV 180  
       || || || || : ||||| : : : || : || ||||| ||||| ||||| || ||  
Db   143 GAASLIFYSLDYARTRLANDAKSAAKKGGERGFNLVDUYRYKTYDSGLRGLRSGEFSV 202  
  
OY    181 OGIIITYRAAYRGVYDTAAAG-MLPEDKNVHIIVSWMAIOSVAVACGLSTPEDTVRRMM 239  
       ||||| : ||||| ||||| : ||||| : ||||| : ||||| : ||||| : |||||  
Db   203 VGIIVYRGLYRFEMDYTLPPVYLVEGLEGNFLSFLIGNAVVTGSGVASYPDLTIERRMM 262  
  
OY   240 QSGRKGDIMVTGTADCWKRIAKDGCAAFEGKGSANVLRCMGGAFAVLYLDEIK 294  
       || : : : : || ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db   263 TSGEA---VKISSPECGROIILAKGCANSFEKGACANINIRGVAGAGVLTIDVOV 314
```

Search completed: November 12, 2002, 16:46:26
Job time : 8.6495 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:43:45 ; Search time 25.2766 Seconds

(without alignments)
2421.054 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553

Sequence: 1 MGDHMSFLKDFLAGAVAAA.....LRMGSAFYLVLYDEIKKYV 297

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1464.5	94.3	298	6	046373
2	1463.5	94.2	298	11	062164
3	1411.5	90.9	298	6	0850H5
4	1377.5	88.7	298	13	09YIC4
5	1377.5	88.7	298	13	09PRH1
6	1374.5	88.5	298	13	09PRH2
7	1366.5	88.0	298	13	09PRH2
8	1245.5	80.2	299	5	0919M9
9	1241.5	79.9	300	5	095VX4
10	1241.5	79.9	299	5	095S30
11	1234.5	79.5	317	13	091336
12	1183	76.2	288	5	044093
13	1183	76.2	288	5	044094
14	1147	73.9	307	5	062526
15	1139.5	73.4	304	5	025129
16	1101.5	70.9	315	4	09H0C2

17	1045.5	67.3	313	5	P91410	P91410 caenorhabd
18	1043.5	67.2	313	5	021103	021103 caenorhabd
19	1037.5	66.8	300	5	045865	045865 caenorhabd
20	1005.5	64.7	300	5	001813	001813 caenorhabd
21	993.5	64.0	300	5	017407	017407 caenorhabd
22	989.5	63.7	309	5	097470	097470 dictyostell
23	959	61.8	307	8	09XM22	09xm22 ascaris suu
24	950	61.2	318	5	09B316	09b316 toxoplasma
25	905.5	58.3	301	5	025692	025692 plasmodium
26	904.5	58.2	301	5	026006	026006 plasmodium
27	841.5	54.2	170	6	09X569	09x569 sus scrofa
28	772	49.7	306	5	018683	018683 caenorhabd
29	757.5	48.8	305	3	09P8M1	09p8m1 yarrowia li
30	750.5	48.3	307	5	076286	076286 trypanosoma
31	748.5	48.2	303	3	074260	074260 candida par
32	746.5	48.1	379	10	049447	049447 arabidopsis
33	745.5	48.0	326	5	P91270	P91270 caenorhabd
34	743.5	47.9	307	5	026697	026697 trypanosoma
35	740.5	47.7	386	10	P93767	P93767 lycopersico
36	738.5	47.6	388	10	049875	049875 lupinus alb
37	731.5	47.1	317	5	09N647	09n647 leishmania
38	728.5	46.9	306	3	P78754	P78754 schizosacch
39	727.5	46.8	331	10	041628	041628 triticum tu
40	708	45.6	305	3	09P876	09p876 pichia jadi
41	705	45.4	305	3	09P875	09p875 pichia jadi
42	698	44.9	308	3	08PFA7	08pfa7 neocallimas
43	681	43.9	330	10	09FM86	09fm86 arabidopsi
44	676	43.5	298	5	021809	021809 caenorhabd
45	659	42.4	262	10	09AVT6	09avt6 picea abies

ALIGNMENTS

RESULT 1

ID	046373	PRELIMINARY:	PRT:	298 AA.
AC	046373:			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	ADP/ATP translocase.			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_Taxid=9986;			
RN	[1]			
RP	SEQUENCE FROM N. A.			
RC	TISSUE=SKLETAL MUSCLE;			
RA	Yamaguchi N., Kasai M.;			
RT	"Identification of a 30kDa calsequestrin-binding protein, which			
RT	regulates calcium release from sarcoplasmic reticulum of rabbit			
RT	skeletal muscle."			
RL	J. Biochem. 335:541-547(1998).			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL			
CC	INNER MEMBRANE (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.			
DR	EMBL: AB009386; BAA23777.1; -.			
DR	InterPro: IPR001993; Mitoch_carrier.			
DR	InterPro: IPR02067; Mit_carrier.			
DR	Pfam: PF00153; mito_carr; 3.			
DR	PRINTS: PR00926; MITOCARRIER.			
DR	PROSITE: PS00215; MITOCH_CARRIER. 3.			
KW	Inner membrane; Mitochondrion; Transmembrane; Transport.			
SO	SEQUENCE 298 AA; 32901 MW; CAEA32C8B164AD78 CRC64;			
Query Match	94.3%:	Score 1464.5:	DB 6:	Length 298;
Best local similarity	94.6%:	Pred. No. 6.2e-126;		
Matches 282:	Conservative 7;	Mismatches 8;	Indels 1;	Gaps 1;
QY	1 MGDHMSFLKDFLAGAVAAVSKTAVAPIERVKLLIQVQHSKQISAKQYKGIIDCVR 60			
Db	1 MSDQSLFKDFLAGVAAVSKTAVAPIERVKLLIQVQHSKQISAKQYKGIIDCVR 60			

QY	1PEKCGFLSEFMNGNLANYRYEPFOALNFAEKDYKOLFGLGVDRHKQWRFEGAGLASG	120
QY	61	1PEKCGFLSEFMNGNLANYRYEPFOALNFAEKDYKOLFGLGVDRHKQWRFEGAGLASG
DB	61	1PEKCGFLSEFMNGNLANYRYEPFOALNFAEKDYKOLFGLGVDRHKQWRFEGAGLASG
QY	121	GAAGATSLCEVYPDLEFARTRLAADYGR-FAQREFHGLGDCIIKIRKSDGLRGLYGFNVS
DB	121	GAAGATSLCEVYPDLEFARTRLAADYGRFAQREFHGLGDCIIKIRKSDGLRGLYGFNVS
QY	180	VGGIIIRRAAYGVYDTAKGMLPDPKKNVHIFPSNMIAQSVTVAVAGLISPEPTVRRRAM
DB	181	VGGIIIRRAAYGVYDTAKGMLPDPKKNVHIFPSNMIAQSVTVAVAGLISPEPTVRRRAM
QY	240	QSGRGADIMYGTATDCWKRIRAKDEGAKAFEGKAMSNTVRGGAFAVLTYDEIKKYV
DB	241	QSGRGADIMYGTATDCWKRIRAKDEGAKAFEGKAMSNTVRGGAFAVLTYDEIKKYV
RESULT 2		
QY	062164	PRELIMINARY; PRT; 298 AA.
AC	062164	
DT	01-NOV-1996	(TREMBlrel. 01. Created)
DT	01-NOV-1996	(TREMBlrel. 01. Last sequence update)
DT	01-JUN-2002	(TREMBlrel. 21. Last annotation update)
DE	Adenine nucleotide carrier (adenine nucleotide translocase 1) (Similar to solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4) (Hypothetical 32.9 kDa protein).	
GN	SLC25A4	OR MAMC1 OR ANTI.
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-BALB/C;	TISSUE=MUSCLE;
RA	Laplace C., Costet P.;	
RL	Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	Ley S.E., Chen Y.-S., Graham B.H., Wallace D.C.;	
RT	"Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes."	
RL	Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RA	Strausberg R.;	
RL	Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.	
RN	[4]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=EYE;	
RA	Strausberg R.;	
RL	Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.	
CC	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).	
CC	-I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.	
DR	EMBL: X74510; CAAS2616.1; -;	
DR	EMBL: AF240002; AAF64470.1; -;	
DR	EMBL: BC003791; AAH03791.1; -;	
DR	EMBL: BC026925; AAH26925.1; -;	
DR	MGI: MGI:1353495; Slc25a4.	
DR	InterPro: IPR001993; MitochCarrier.	
DR	InterPro: IPR002067; MLCCarrier.	
DR	Pfam: PF00153; mito_carr.3.	
DR	PRINTS: PRO00926; MITOCARRIER.	
DR	PROSITE: PS00215; MITOCH_CARRIER; 3.	
KW	Hypothetical protein; Inner membrane; Repeat; Transmembrane; Transport; Mitochondrion.	
SO	SEQUENCE	298 AA; 32904 MW; 3A849FEABD981462 CRC64;
Query Match 94.2%; Score 163.5; DB 11; Length 298;		
Best Local Similarity 94.0%; Pred. No. 7.7e-126;		
Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 14;		

ID	QYVICA	PRELIMINARY:	PRT:	298 AA.
QY	1	MDHAMSFLKDLACGAAVAAAVSKTAVAPLERKLLLOVOHASKOISAEQYGGIIDCVYR	60	
Db	1	MDQALSTFLKDLACGIAAASVSKTAAAPLERKLLLOVOHASKOISAEQYGGIIDCVYR	60	
QY	61	IRKEGGLSTFWMKGNLANVIRYFPTQALNFAFDKXKQIFLGVDVDRHKQFWRFFAGNLASG	120	
Db	61	IRKEGGLSTFWMKGNLANVIRYFPTQALNFAFDKXKQIFLGVDVDRHKQFWRFFAGNLASG	120	
QY	121	GAGATSTLCFVYPLDFAPTRLAADYGR-RAQREPHGLDGCITIKRSDGLRGLYGFNVS	179	
Db	121	GAGATSTLCFVYPLDFAPTRLAADYGVKSSQREDFNGLDGLTKRIFKSDGLKGLYGFNVS	180	
QY	180	VGGIITTYRAAYGVYDTAKGMLPDPKNVHIYFSWMIAGSVTAAGVGLSTSPPTVRRRMM	239	
Db	181	VGGIITTYRAAYGVYDTAKGMLPDPKNVHIYFSWMIAGSVTAAGVGLSTSPPTVRRRMM	240	
QY	240	QSGRGADIMYGTVDCKWKRIAKDEGAKAFFGAGSNVLRGNGAFVLYLDEIKKY	296	
Db	241	QSGRGADIMYGTVDCKWKRIARDEGAKAFFGAGSNVLRGNGAFVLYLDEIKKF	297	
RESULT 4				
ID	QYVICA	PRELIMINARY:	PRT:	298 AA.
QY	1	MDHAMSFLKDLACGAAVAAAVSKTAVAPLERKLLLOVOHASKOISAEQYGGIIDCVYR	60	
Db	1	MDQALSTFLKDLACGIAAASVSKTAAAPLERKLLLOVOHASKOISAEQYGGIIDCVYR	60	
QY	61	IRKEGGLSTFWMKGNLANVIRYFPTQALNFAFDKXKQIFLGVDVDRHKQFWRFFAGNLASG	120	
Db	61	IRKEGGLSTFWMKGNLANVIRYFPTQALNFAFDKXKQIFLGVDVDRHKQFWRFFAGNLASG	120	
QY	121	GAGATSTLCFVYPLDFAPTRLAADYGR-RAQREPHGLDGCITIKRSDGLRGLYGFNVS	179	
Db	121	GAGATSTLCFVYPLDFAPTRLAADYGVKSSQREDFNGLDGLTKRIFKSDGLKGLYGFNVS	180	
QY	180	VGGIITTYRAAYGVYDTAKGMLPDPKNVHIYFSWMIAGSVTAAGVGLSTSPPTVRRRMM	239	
Db	181	VGGIITTYRAAYGVYDTAKGMLPDPKNVHIYFSWMIAGSVTAAGVGLSTSPPTVRRRMM	240	
QY	240	QSGRGADIMYGTVDCKWKRIAKDEGAKAFFGAGSNVLRGNGAFVLYLDEIKKY	296	
Db	241	QSGRGADIMYGTVDCKWKRIARDEGAKAFFGAGSNVLRGNGAFVLYLDEIKKF	297	

```

RT      Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
RL      a sex-linked gene, Adp/Atp translocase." ;
RL      Mol. Biol. Evol. 15:1612-1619(1998).
CC      -1- SUBCELLULAR LOCATION: INTERMEMBRANE PROTEIN, MITOCHONDRIAL
CC      -1- INNER MEMBRANE (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR      EMBL; AB008463; BAA36513.1; -
DR      EMBL; AB008456; BAA36506.1; -
DR      EMBL; AB008461; BAA36511.1; -
DR      EMBL; AB008462; BAA36512.1; -
DR      InterPro: IPR001993; Mitoch_carrier.
DR      InterPro: IPR002067; Mit_carrir.
DR      InterPro: IPR002030; Mit_uncoupling.
DR      Pfam: PFO0153; mito_carr_3.
DR      PRINTS: PR00926; MITOCARRIER.
DR      PRINTS: PR00784; MTUNCOUPLING.
DR      PROSITE: PS00215; MITOCH_CARRIER_3.
KW      Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ      SEQUENCE 298 AA; 33054 MW; B0E23AD56F54BD36 CRC64;

Query March 88.7%: Score 1377.5; DB 13; Length 298;
Best Local Similarity 86.6%: Pred. No. 5.7e-118;
Matches 258; Conservative 23; Mismatches 16; Indels 1; Gaps

QY      1 MGDHWSFLDPLAGAAVAAVSTAAVAPIERVYLLQVQHASKOISAEKQYKGIIDCVVR 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      1 MTDAAISFADFLAGGVAAAIISTVAPIERVYLLQVQHASKOITADKQYKGIIDCVVR 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      61 IPKEDGFLSWRGNLNVIRYPTQALNFAEKDKYKQLFLGSGVDRHKQFWRYFAGNLASG 120
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Oy		121	GAAATSLCYYPLDPAKTLADVGR-AQRFHBLGCIITIKRSDGLRELYGFNVS	179
Dd		121	GAAATSLCYYPYLPDEFARTLADVAKAGADRERFKLGCLIAKRFSBKLXYGVFNVS	180
Oy		180	VQGIIIRAYAFVGYPDRAKMLDPKNVHFYSMMTASVTAVAGLLSPEDTVRRRAM	239
Dd		181	VQGIIRRAYAFGYIDPARKMLDPKPNTHTIFISMTLAQTVAIVAGFASPPTVRRRAM	240
Oy	240	OSGRKKADMGTCTVDGCWKRIANDECAKAFFKGAMSNVLRGMGAPVLYLVDELKRYV	297	
Dd	241	QSGRKGAEMYSGITDCWKKIARIDESRAFEGKAMSNNVLRGMGAFPVLYLVDELKRYI	298	

RESULT 6
O9PRH2 PRELIMINARY; PRT; 298 AA.

```

AC O9PRH2;
DT 01-MAY-2000 (TREMBLrel_13, Created)
DT 01-MAY-2000 (TREMBLrel_13, Last sequence update)
DI 01-Mar-2002 (TREMBRel_10, last annotation update)
DS ADP/ATP translocase.
SE Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphiibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxId=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=990634429; PubMed=9866197; Mura I., Ohnishi H., Nakamura M., Ichikawa Y., Saitoh K.; "The origin and differentiation of the heteromorphic sex chromosomes Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of a sex-linked gene, Adp/ATP translocase."; Mol. Biol. Evol. 15:1612-1619(1998).
RL -01 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
CC -1 SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL AB008460; BAA36510.1; -.
DR EMBL AB008458; BAA36508.1; -.
DR EMBL AB008459; BAA36509.1; -.
DR InterPro IPRO001993; Mitoch_carrier.
DR InterPro IPRO02067; Mt_c Carrier.
    
```

DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KM Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;

Query Match 88.5%; Score 1374.5; DB 13; Length 298;
 Best Local Similarity 86.2%; Pred. No. 1,le-117;
 Matches 257; Conservative 24; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVADIERVKLLQVOHASKQISAEKQYKGIIDCVVR 60
 DB 1 MTDAAISFAKDFLAGVAANAISKTAVADIERVKLLQVOHASKQITADKHKGIMDCVVR 60
 QY 1PKKGFSEFWRGNLANIYRFPQALNFARFKDKYKQFLGVDNRHKOFRYFAGNLSG 120
 DB 1PKKGFSEFWRGNLANIYRFPQALNFARFKDKYKQFLGVDNRHKOFRYFAGNLSG 120
 QY 121 GAAGATSLCFEYVPLDFARTRLADVGR-AQREFHGLGDCIIRKFSKGLGXYGFNV 179
 DB 121 GAAGATSLCFEYVPLDFARTRLADVGRAGADREFKGLGDCIIRKFSKGLGXYGFNV 180
 QY 180 VQGIITRAAFYGYDTAKGMLPDPKKNHIFVSMIAQSVTAAGLSYPTDYRRMM 239
 DB 181 VQGIITRAAFYGYDTAKGMLPDPKKNHIFISWMIAGTVTAAGFASYPDYRRMM 240
 QY 240 QSGRKGADIMTGVDCRRTAKDEGAKAFKGAAMSNVLRMGAFVLYLDEIKKY 297
 DB 241 QSGRKGAEIMTGVTDCKKTLARDEGSAFEGKAMSNVLRMGAFVLYLDEIKKY 298

RESULT 7

Q919M9 PRELIMINARY; PRT; 298 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Adenine nucleotide translocase.
 GN ANTL.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Crawford M.J., Khosrowshahian F., Varmuza S.L., Livsage R.A.;
 RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
 RT Dynamic Patterns of Expression During Development."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF31347; AAF63471.1; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KM Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;

Query Match 88.0%; Score 1366.5; DB 13; Length 298;
 Best Local Similarity 86.2%; Pred. No. 5,8e-117;
 Matches 257; Conservative 23; Mismatches 17; Indels 1; Gaps 1;
 QY 1 MGDHMSFLKDFLAGAANAASKTAVADIERVKLLQVOHASKQISAEKQYKGIIDCVVR 60
 DB 1 MTDAAISFAKDFLAGVAANAISKTAVADIERVKLLQVOHASKQITADKHKGIMDCVVR 60

DB 1 MTDAAISFAKDFLAGVAANAISKTAVADIERVKLLQVOHASKQITADKHKGIMDCVVR 60
 QY 1PKKGFSEFWRGNLANIYRFPQALNFARFKDKYKQFLGVDNRHKOFRYFAGNLSG 120
 DB 1PKKGFSEFWRGNLANIYRFPQALNFARFKDKYKQFLGVDNRHKOFRYFAGNLSG 120
 QY 121 GAAGATSLCFEYVPLDFARTRLADVGR-AQREFHGLGDCIIRKFSKGLGXYGFNV 179
 DB 121 GAAGATSLCFEYVPLDFARTRLADVGRAGADREFKGLGDCIIRKFSKGLGXYGFNV 180
 QY 180 VQGIITRAAFYGYDTAKGMLPDPKKNHIFVSMIAQSVTAAGLSYPTDYRRMM 239
 DB 181 VQGIITRAAFYGYDTAKGMLPDPKKNHIFISWMIAGTVTAAGFASYPDYRRMM 240
 QY 240 QSGRKGADIMTGVDCRRTAKDEGAKAFKGAAMSNVLRMGAFVLYLDEIKKY 297
 DB 241 QSGRKGADIMTGVTDCKKTLARDEGSAFEGKAMSNVLRMGAFVLYLDEIKKY 298

RESULT 8

Q95VX4 PRELIMINARY; PRT; 299 AA.

DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ADP-ATP translocator.
 OS Ethmostigmus rubripes.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Myriapoda; Chilopoda;
 OC Pleurostigmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
 OX NCBI_TaxID=62613;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Burnell J.N.;
 RT "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus
 RT rubripes."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF401758; AAL02100.1; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN.2.
 SQ SEQUENCE 299 AA; 33037 MW; 3C3BBCB26E7C3C5E CRC64;

Query Match 80.2%; Score 1245.5; DB 5; Length 299;
 Best Local Similarity 80.3%; Pred. No. 7e-106;
 Matches 236; Conservative 25; Mismatches 32; Indels 1; Gaps 1;

QY 5 AWSFLKDFLAGAANAASKTAVADIERVKLLQVOHASKQISAEKQYKGIIDCVVRIPKE 64
 DB 5 AVSFLKDFIAGVAANAISKTAVADIERVKLLQVOHASKQIADVQKGMVDCVVRIPQOE 64
 QY 65 QGFLSFWRGNLANIYRFPQALNFARFKDKYKQFLGVDNRHKOFRYFAGNLSGGAAG 124
 DB 65 QGILSYWRGNLANIYRFPQALNFARFKDKYKQFLGVDNRHKOFRYFAGNLSGGAAG 124
 QY 125 ATSLCFEYVPLDFARTRLADVGR-AQREFHGLGDCIIRKFSKGLGXYGFNVYOGI 183
 DB 125 ATSLCFEYVPLDFARTRLADVGRAGADREFKGLGDCIIRKFSKGLGXYGFNVYOGI 184
 QY 184 IYRAAFYGYDTAKGMLPDPKKNHIFVSMIAQSVTAAGLSYPTDYRRMMOSGR 243
 DB 185 IYRAAFYGYDTAKGMLPDPKKNHIFVSMIAQSVTAAGLSYPTDYRRMMOSGR 244
 QY 244 KGADIMTGVDCRRTAKDEGAKAFKGAAMSNVLRMGAFVLYLDEIKKY 297
 DB 245 KKADILYNTIDCWGKIYKTEGGAFFKGAAPSNILRGTGAFVLYLDEIKALI 298

RESULT 9

Q9NHM5 PRELIMINARY; PRT; 300 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)

RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY:
 RA Stapleton M., Brokstein P., Hong L., Abbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA Gerardo R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Paoletti J., Paragas V., Park S.,
 RA Patel S., Phouanemavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Cealnikar S.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY060978; AAL28526.1; -
 DR EMBL: AY070894; AAL48516.1; -
 DR FlyBase: FBgn0003360; sesh.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carri; 3.
 DR PROSITE: PS00215; MITOCH_CARRIER, UNKNOWN_3.
 SO SEQUENCE 299 AA; 32909 MW; D51F3E2A70BD59E8 CRC64;

Query Match 79.9%; Score 1241; DB 5; Length 299;
 Best Local Similarity 79.7%; Pred. No. 1,8e-105;
 Matches 232; Conservative 26; Mismatches 33; Indels 0; Gaps 0;

QY 5 AMSFLKDFELACAAVAANAASKTAVAPREPERKLLVOHNAKSOTSAEKQYGIIDCVYRIKPE 64
 Db 7 AVGEFKDFEPAAGGISAASKTAVAPERKLLVOHNSKQISPDQKGMVDFCIRIPE 66
 QY 65 QGFLSFNMGNLANYIRFPTQALNFAEFKDKYKQLFLGVDSDHKKQFRRFAGNLASGGAAG 124
 Db 67 QGFSEFNMGNLANIYRFPQALNFAEFKDKYKQVFLGVDKNTQFWRFFAGNLASGGAAG 126
 QY 125 ATSLCFVYPLDPARTRLADYGRRAQREFHGLDCTIKIFKSDGIRGLYQGFNWSVGIT 184
 Db 127 ATSLCFVYPLDPARTRLADYGRRAQREFHGLDCTIKIFKSDGIRGLYQGFNWSVGIT 186
 QY 185 IYRAAFEGVYPTARGMLDPPKRVNHFEVSMWMTAOSTVAVAGLSYFEDVRRRRMMQSGRK 244
 Db 187 IYRAAFEGVYPTARGMLDPPKRVNPTIYSLMAQVYTVTAIGVSTPFDVRRRRMMQSGRK 246
 QY 245 GADIMYTTGVDCWRKIRAKDEGAKAFKFGAMSGNVLRGMSGAFVLYLDEIKK 295
 Db 247 ATEVIYKNTLTMGWATIAKQEGTGAFKFAFNSILRGITGCAVLYLDEIKK 297

RESULT 11
 Q91336 PRELIMINARY; PRT; 317 AA.
 ID Q91336 AC Q91336.
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana sylvatica (wood frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 OX NCBI_TaxID=45438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE=LIVER.
 RC MEDLINE-97398141; PubMed-925666;
 RX Cal Q., Greenway S.C., Storey K.B.;
 RA "Differential regulation of the mitochondrial ADP/ATP translocase gene
 in wood frogs under freezing stress.";
 RT Biochim. Biophys. Acta 1353:69-78(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP TISSUE=LIVER.
 RC Cal Q., Storey K.B.;
 RA Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: U04832; AA97/882.2; -
 DR InterPro: IPR001993; Mitoch_carrier.

DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCH_CARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SO SEQUENCE 317 AA; 35005 MW; 5F66B7EDBD5CEB72 CnC64;

Query Match 79.5%; Score 1234.5; DB 13; Length 317;
 Best Local Similarity 85.7%; Pred. No. 7.6e-105;
 Matches 233; Conservative 21; Mismatches 17; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGVAAVSTAVAPIERKLLQVOHASKQISAQKQYGIIDCVYR 60
 DB 1 MTDANMSFAKDFLAGVAAVSTAVAPIERKLLQVOHASKQITAAQKQYGIIDCVYR 60
 QY 61 IPKEGFLSFMRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKKQFMRFAGNLASG 120
 DB 61 IPKEGFLSFMRGNLANVIRYPTQALNFGFKDKYKQFLGVDNRHKKQFMRFAGNLASG 120
 QY 121 GAAGATSLCFYVPLDFARTRLADYGR-AOREFHGLSDCIKIKPSDGLRGLYGFNV 179
 DB 121 GAAGATSLCFYVPLDFARTRLADYGRAGAGREFNGDLCKIKPSDGLRGLYGFNV 180
 QY 180 VQGIITVAAAFYGYDTAKGMLPDKNVHIFYSWMIASVTAVAGLSYPTVRRMM 239
 DB 181 VQGIITVAAAFYGYDTAKGMLPDKNVHIFYSWMIASVTAVAGLSYPTVRRMM 240
 QY 240 QSGRKADIMYTGIVDCWKRIKADGAKAFK 271
 DB 241 QSGRKALIMYSGTIDCKKRIADGGRAFR 272

RESULT 12
 044093 PRELIMINARY; PRT; 288 AA.
 ID 044093:
 AC 044093:
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ADP/ATP translocase (Fragment).
 GN SESB.
 OS Drosophila pseudoobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7237;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zeng L.-W., Comeron J.M., Chen B., Kretzman M.;
 RL Genetics 0:0-0(1997).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF025798; AAB87883.1; -
 DR FlyBase: FBgn0023292; DpseVesB.
 DR InterPro: IPR001993; Mitoch_carr.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCH_CARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 FT NON_TER 288
 FT SEQUENCE 288 AA; 31725 MW; 052B0CC0050436B0 CnC64;

Query Match 76.2%; Score 1183; DB 5; Length 288;
 Best Local Similarity 79.6%; Pred. No. 3.5e-100;
 Matches 226; Conservative 25; Mismatches 31; Indels 2; Gaps 2;

QY 5 AMSFLKDLGAVAAVSTAVAPIERKLLQVOHASKQISAQKQYGIIDCVYR 64
 DB 7 AIGFVKDPAAGISAASVSTAVAPIERKLLQVOHASKQISPDQYGMVDCFRIRKE 66
 QY 65 QGFLSFMRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKKQFMRFAGNLASG 124

DB 67 QGFSFMRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKKQFMRFAGNLASG 126
 QY 125 ATSLCFYVPLDFARTRLADYGRARQREFHGLDCCIIFKPSDGLRGLYGFNVSGIT 184
 DB 127 ATSLCFYVPLDFARTRLADYGRARQREFHGLDCCIIFKPSDGLRGLYGFNVSGIT 186
 QY 185 IYRAVFGYVDTAKGMLPDKNVHIFYSWMIASVTAVAGLSYPTVRRMMQSGRK 244
 DB 187 IYRAVFGYVDTAKGMLPDKNVHIFYSWMIASVTAVAGLSYPTVRRMMQSGRK 245
 QY 245 GADIMYTGIVDCWKRIKADGAKAFKAGMSVLRGKAGATV 288
 DB 246 ATEIITKNTLHMCATIAQKQS-AFFKAGFNSVLRGTGATV 288

RESULT 13
 044094 PRELIMINARY; PRT; 288 AA.
 ID 044094:
 AC 044094:
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ADP/ATP translocase (Fragment).
 GN SESB.
 OS Drosophila subobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7241;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zeng L.-W., Comeron J.M., Chen B., Kretzman M.;
 RL Genetics 0:0-0(1997).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF025799; AAB87884.1; -
 DR FlyBase: FBgn0023237; DsubVesB.
 DR InterPro: IPR001993; Mitoch_carr.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCH_CARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 FT NON_TER 288
 FT SEQUENCE 288 AA; 31775 MW; 06A1DE477E81B26 CnC64;

Query Match 76.2%; Score 1183; DB 5; Length 288;
 Best Local Similarity 79.6%; Pred. No. 3.5e-100;
 Matches 226; Conservative 23; Mismatches 33; Indels 2; Gaps 2;

QY 5 AMSFLKDLGAVAAVSTAVAPIERKLLQVOHASKQISAQKQYGIIDCVYR 64
 DB 7 AMGFVKDPAAGISAASVSTAVAPIERKLLQVOHASKQISPDQYGMVDCFRIRKE 66
 QY 65 QGFLSFMRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKKQFMRFAGNLASG 124
 DB 67 QGFSFMRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKKQFMRFAGNLASG 126
 QY 125 ATSLCFYVPLDFARTRLADYGRARQREFHGLDCCIIFKPSDGLRGLYGFNVSGIT 184
 DB 127 ATSLCFYVPLDFARTRLADYGRARQREFHGLDCCIIFKPSDGLRGLYGFNVSGIT 186
 QY 185 IYRAVFGYVDTAKGMLPDKNVHIFYSWMIASVTAVAGLSYPTVRRMMQSGRK 244
 DB 187 IYRAVFGYVDTAKGMLPDKNVHIFYSWMIASVTAVAGLSYPTVRRMMQSGRK 245
 QY 245 GADIMYTGIVDCWKRIKADGAKAFKAGMSVLRGKAGATV 288
 DB 246 ATEIITKNTLHMCATIAQKQS-AFFKAGFNSVLRGTGATV 288

	RESULT	14
ID	062526	PRELIMINARY; PRT: 307 AA.
AC	062526;	
DT	01-AUG-1998 (TrEMBLrel. 07, Created)	
DR	01-AUG-1998 (TrEMBLrel. 07, Last sequence update)	
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)	
DE	AMT2 protein.	
GN	AMT2 OR CG1683.	
OS	Drosophila melanogaster (fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Ephyroidae; Drosophilidae; Drosophila.	
OX	NCBI_TaxID=1227;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-BERKELEY.	
RX	MEDLINE=20196006; PubMed=10731132;	
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,	
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,	
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,	
RA	Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,	
RA	Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,	
RA	Arril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,	
RA	Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	
RA	Beeson K.Y., Benos P.V., Bertram B.P., Bhargava D., Bolshakov S.,	
RA	Borkova D., Botchan M.R., Bouck T.J., Brokstein P., Brotlier P.,	
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,	
RA	de Pablos B., Delcher A., Deng Z., Duan R.D., Dew I., Dietz S.M.,	
RA	Dodson K., Douc L.E., Downes M., Mayas-Rocha S., Dunkov B.C., Dunn P.,	
RA	Durbin K.J., Evangelista C.C., Ferraz A.C., Ferreira S., Fleischmann W.,	
RA	Fowler C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,	
RA	Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,	
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,	
RA	Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,	
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,	
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,	
RA	Merklov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,	
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,	
RA	Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Pacile J.M.,	
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Putl V., Reese M.G.,	
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,	
RA	Shue B.C., Sidenklamos I., Simpson M., Skupski M.P., Smith T.,	
RA	Soler E., Spralling A.C., Stapleton M., Strong R., Sun E.,	
RA	Strizaks R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,	
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,	
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,	
RT	"The genome sequence of Drosophila melanogaster."	
RL	Science 287:2185-2195(2000).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-OREGON-R;	
RL	Submitted (MAR-1998) to the EMBL/genbank/DBD databases.	
DR	EMBL: AE003484; AAF47956.1; -	
DR	EMBL: Y10618; CAAT1629.1; -	
DR	FLYBase: FBgn002511; Amt2.	
DR	InterPro: IPRO01993; Mitoch.carrier.	
DR	InterPro: IPRO02067; Mit_carrier.	
DR	Pfam: PF00153; mito-carri-3.	
DR	PRINTS: PR00926; MITOCARRIER.	
DR	PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_2.	
SO	SEQUENCE 307 AA; 33744 MW; 3DB3DPED82061C CRC64;	

Matches	214	Conservative	33	Mismatches	43	Indels	0	Gaps	0
QY	7	SLKLPFLAGAAVAAVSKTAVAPIERVKLLLOVQHSKQISAEKQYKGIIDCVRRIPKEQG	66		1				
Db	17	SFLMDPMGCVSAALAKTAVAPIERVKLLLOVQHSKQISAEKQYKGIIDCVRRIPKEQG	76		1				
QY	67	FLSPFGRGNLANVIRFEPQALNFARDKQKFLFSGVDHKKQFWRFPGNLAGSGAAGT	126		1				
Db	77	FSSEFGRGNLANVIRFEPQALNFARDKQKFLFSGVDHKKQFWRFPGNLAGSGAAGT	136		1				
QY	127	SLCFEYPLDFAFTRLAADVGRAROREFHGLDCCIIEFKSPDRLRGLYOGFNVSVGGIITY	186		1				
Db	137	SLCFEYPLDFAFTRLAADVGRAROREFHGLDCCIIEFKSPDRLRGLYOGFNVSVGGIITY	196		1				
QY	187	RAAYGCVDTAKGLPDPKNNVHIEVSWMIAQSVTAVALISYPDTVRRRMQSGRKGA	246		1				
Db	197	RAAYGCVDTAKGLPDPKNNVHIEVSWMIAQSVTAVALISYPDTVRRRMQSGRKGA	256		1				
QY	247	DIMYGYDQCMRKIAKDEGAKAFEGGANSNVLRGGAFAVLVLYDEIKY	296		1				
Db	257	EMVYKNTAHCMVLIAKQEGIGAFEGGALSNIIRGTGALVLYALYDEMKY	306		1				
RESULT 15									
ID	Q25129	PRELIMINARY:	PRT:	304	AA.				
AC	Q25129.								
DT	01-NOV-1996	(TREMblrel. 01, Created)							
DT	01-NOV-1996	(TREMblrel. 01, Last sequence update)							
DT	01-MAR-2002	(TREMblrel. 20, Last annotation update)							
DE	ADP/ATP translocase.								
GN	HRATL1.								
OS	Halocynthia roretzi (Sea squirt).								
OC	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;								
OC	Stolidobranchia; Pyuridae; Halocynthia.								
OX	NCBI_TaxID=7729;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RA	Mya T.;								
RL	Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.								
RL	[2]								
RP	SEQUENCE FROM N.A.								
RA	Mya T., Makabe K., Satoh N.;								
RT	"Expression of a gene for major mitochondrial protein, ADP/ATP								
RT	translocase, during embryogenesis in the ascidian Halocynthia								
RT	roretzi.";								
RL	Dev. Growth Differ. 36:39-48(1994).								
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL								
CC	INNER MEMBRANE (By Similarity).								
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.								
DR	EMBL; D83069; BAAL1765.1; "								
DR	InterPro: IPR001993; Mitoch_carrier.								
DR	InterPro: IPR002067; Mlt_carrier.								
DR	Pfam: PF00153; mlt_carrier_3								
DR	PRINTS; PR00926; MITOCH_CARRIER.								
DR	PROSITE; PS00215; MITOCH_CARRIER; 3.								
KW	Inner membrane; Mitochondrion; Transmembrane; Transport.								
SW	SEQUENCE 304 AA; 33307 MW; 51FD0D7DEB654880 CRC64;								
Query Match 73.4%; Score 1139.5; DB 5; Length 304;									
Best Local Similarity 74.6%; Freq. No. 3.6e-96;									
Matches 220; Conservative 18; Mismatches 54; Indels 3; Gaps 14;									
QY	6	WS---FLKDFLAGAAVAAVSKTAVAPIERVKLLLOVQHSKQISAEKQYKGIIDCVRRIP	62		1				
Db	3	WSAVDFADDLAIGGTAALAKTAVAPIERVKLLLOVQAVSTOMKAGTEKGIITDAFVRIP	62		1				
QY	63	KEQGLSLFWGRGNLANVIRFEPQALNFARFKDYKQLFLGVDHKKQFWRFPGNLAGSGA	122		1				
Db	63	KEQGFSLFWGRGNLANVIRFEPQALNFARFKDYKQLFLGVDHKKQFWRFPGNLAGSGA	122		1				

Wed Nov 13 10:40:33 2002

us-09-393-441-31.rsp

Page 8

Db	123	AGATGTCFVYPLDFAFRTPLRIADIGSGSPOETGTCGNCLATIVKDKDPRGLYGFVYSIQG	182
Qy	183	IIIRAAVEFGYDPAKAGLDPKPKVHVEFVSMINOSTAAVAGLLSYEPDFVRRRRMMQSG	242
Db	183	IIIVRAAFEGYIDYKGLKDPKQPTPLIVSHALNQVTTGAGLISYDFVIVRRRRMMQSG	242
Qy	243	RKGDIMVTGIVDCKRIINADDEGAKAPFKGMSVNLFGMGAGFVLYLYDEIKTV	297
Db	243	RNKEKRMATKGVLDWGMKILYKGGKRAFFKGLSNLIVIGTGGALVLVLYIDELKTLV	297

Search completed: November 12, 2002, 16:47:49
Job time : 27.2766 secs

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI Ghosh SS;
XX
XX MPI: 2000-365619/31.
DR N-PSDB: AAD00520.
XX
PT Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease -
XX
PS Claim 45; Page 172-173; 175pp; English.
XX
XX The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT2 from human brain.
XX
SQ Sequence 298 AA:

Query Match 100.0%; Score 1547; DB 21; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.5e-154;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSFKDPDLGAGVAAAIKSTAVAPIERVKLLQOVHASKQITADQYGIIDCVVR 60
DB 1 MTDALSFKDPDLGAGVAAAIKSTAVAPIERVKLLQOVHASKQITADQYGIIDCVVR 60
QY 61 IRKEDEVLSFMRGNLANVIRYPTQALNFAFDKXKQIFLGVDKTKQWRFPAGLASG 120
DB 61 IRKEDEVLSFMRGNLANVIRYPTQALNFAFDKXKQIFLGVDKTKQWRFPAGLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLAADVKGAGAREFRGLGCLVKIKYSDIKGLYGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTRLAADVKGAGAREFRGLGCLVKIKYSDIKGLYGFNVS 180
QY 181 VGGIITRAAYFGIYDTAKGMLPDPKNTIHIVISWMAIQVTVAVAGLTSYPPFTVRRMM 240
DB 181 VGGIITRAAYFGIYDTAKGMLPDPKNTIHIVISWMAIQVTVAVAGLTSYPPFTVRRMM 240
QY 241 QSGRKGTDMYTGTLDCWKRKIARDEGKAFKFGAMSNTVLRGAGAFVLYLDEIKKYYT 298
DB 241 QSGRKGTDMYTGTLDCWKRKIARDEGKAFKFGAMSNTVLRGAGAFVLYLDEIKKYYT 298

RESULT 2
AAU01199
ID AAU01199 standard; Protein; 298 AA.
AC
XX AAU01199;
XX
XX 07-SEP-2001 (first entry)
DE Human adenine nucleotide translocator-2 (ANT-2) protein.
XX
XX Human adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
KW mitochondrial permeability transition pore component; cell survival;
KW mitochondrial core component; mitochondrial related disorder; cancer;
KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
XX

OS Homo sapiens.
XX
XX WO200132876-A2.
XX
XX 10-MAY-2001.
XX
XX 03-NOV-2000; 2000MO-US30535.
XX
XX 03-NOV-1999; 99US-0434354.
XX
XX (MITO-) MITOKOR.
XX
XX Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Erigeri LG;
PI Velicelebi G, Davis RE;
XX
XX MPI: 2001-291054/30.
DR N-PSDB: AAS05902.
XX
XX New nucleic acid expression constructs, useful for screening for agents
PT that alter mitochondrial permeability transition (MPT), comprises
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
PT fused to energy transfer molecule -
XX
PS Disclosure; Fig 2: 186pp; English.
XX
XX The present sequence represents human adenine nucleotide translocator-2
CC (ANT-2) protein. ANT proteins are mitochondrial permeability
CC transition (MPT) pore components responsible for mediating transport
CC of ADP across the mitochondrial inner membrane. ANT proteins interact
CC with other mitochondrial core components e.g. cyclophilins to
CC regulate MPT. The present invention relates to a novel nucleic acid
CC expression construct comprising a promoter operably linked to a
CC polynucleotide encoding a mitochondrial pore component polypeptide
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
CC expression construct can alter mitochondrial membrane permeability
CC transition and/or alter the interaction between mitochondrial core
CC components. The methods are useful for screening for agents that alter
CC MPT and/or cell survival. These agents are useful for the prevention or
CC treatment of diseases associated with altered mitochondrial function or
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC mitochondrial encephalopathy, lactic acidosis, stroke,
CC hyperproliferative disorders e.g. cancer, and deafness.
XX
SQ Sequence 298 AA:

Query Match 100.0%; Score 1547; DB 22; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.5e-154;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSFKDPDLGAGVAAAIKSTAVAPIERVKLLQOVHASKQITADQYGIIDCVVR 60
DB 1 MTDALSFKDPDLGAGVAAAIKSTAVAPIERVKLLQOVHASKQITADQYGIIDCVVR 60
QY 61 IRKEDEVLSFMRGNLANVIRYPTQALNFAFDKXKQIFLGVDKTKQWRFPAGLASG 120
DB 61 IRKEDEVLSFMRGNLANVIRYPTQALNFAFDKXKQIFLGVDKTKQWRFPAGLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLAADVKGAGAREFRGLGCLVKIKYSDIKGLYGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTRLAADVKGAGAREFRGLGCLVKIKYSDIKGLYGFNVS 180
QY 181 VGGIITRAAYFGIYDTAKGMLPDPKNTIHIVISWMAIQVTVAVAGLTSYPPFTVRRMM 240
DB 181 VGGIITRAAYFGIYDTAKGMLPDPKNTIHIVISWMAIQVTVAVAGLTSYPPFTVRRMM 240
QY 241 QSGRKGTDMYTGTLDCWKRKIARDEGKAFKFGAMSNTVLRGAGAFVLYLDEIKKYYT 298
DB 241 QSGRKGTDMYTGTLDCWKRKIARDEGKAFKFGAMSNTVLRGAGAFVLYLDEIKKYYT 298

RESULT 3

AAU10379
 ID AAU10379 standard; Protein: 298 AA.
 AC AAU10379;
 DT 14-FEB-2002 (first entry)
 DE Human adenine nucleotide translocator 2 (ANT2).
 KW Human; adenine nucleotide translocator; ANT; ss;
 KM mitochondrial matrix protein.
 OS Homo sapiens.
 PN WO200185944-A2.
 PD 15-NOV-2001.
 PF 11-MAY-2001; 2001WO-US15416.
 PR 11-MAY-2000; 2000US-0569327.
 PA (MITO-) MITOKOR.
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
 PI Ghosh SS, Moos WH, Pel Y, Carroll AK;
 DR WPI: 2002-055598/07.
 DR N-PSDB; AAS16689.
 PS Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide -
 XX
 XX
 PS Claim 44; Fig 2; 147pp; English.
 CC The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT2.
 CC
 XX
 SQ Sequence 298 AA:
 Query Match 100.0%; Score 1547; DB 23; Length 298;
 Best Local Similarity 100.0%; Pred. No. 2.5e-154;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MPTDAALSFPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKQYKGIICVVR 60
 DB 1 MPTDAALSFPAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKQYKGIICVVR 60
 OY 61 IPKEQEVLSFWRGNLNVIKRYPTQALNFAFKDKYKQIFLGVDKRTQEFWRYPAGNLASG 120
 DB 61 IPKEQEVLSFWRGNLNVIKRYPTQALNFAFKDKYKQIFLGVDKRTQEFWRYPAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLADVGKACAEERFRLGCTLVKTYISDGIKGIYQGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGKACAEERFRLGCTLVKTYISDGIKGIYQGFNVS 180
 OY 181 VOGIITRYRAAYFGIYDTAKGMLPDPKNTHTIVSMIAQVTAVAGLTSTYPTDVRRRMM 240

DB 181 VOGIITRYRAAYFGIYDTAKGMLPDPKNTHTIVSMIAQVTAVAGLTSTYPTDVRRRMM 240
 OY 241 QSGRKGTDIWYGTGLDCWRKRIARDEGKAFKGCAMSVNLKMGAPVLVYDEIKKYY 298
 DB 241 QSGRKGTDIWYGTGLDCWRKRIARDEGKAFKGCAMSVNLKMGAPVLVYDEIKKYY 298
 RESULT 4
 ID AAU1033 standard; Protein: 298 AA.
 AC AAU1033;
 DT 29-AUG-2000 (first entry)
 DE Human adenine nucleotide translocator ANT3.
 KW Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; noctropic;
 KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
 KW antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.
 OS Homo sapiens.
 PN WO200026370-A2.
 PD 11-MAY-2000.
 PF 03-NOV-1999; 99WO-US25883.
 PR 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 PA (MITO-) MITOKOR.
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
 PI Ghosh SS;
 DR WPI: 2000-365619/31.
 DR N-PSDB; AAD00521.
 PS Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 XX
 PS Claim 46; Page 173-174; 175pp; English.
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT3 from human brain.
 CC
 XX
 SQ Sequence 298 AA:

Query Match	94.0%	Score 1454	DB 21	Length 298
Best Local Similarity	92.6%	Fred. No. 1.5e-144		
Matches 274	Conservative 13	Mismatches 9	Indels 0	Gaps 0
Oy	1	MDALSPFAKDDLAGGVAATAIKSTVAPLERVKLLLOVOHASKQJLADQYKGIIDCVYR	60	
Db	1	MTEQATISRAKDDPLAAGIAAISKTVAPLERVKLLLOVOHASKQJLADQYKGIIDCVYR	60	
Oy	61	IPKEDEVLSFWRGNNLANVIRYEPFQALNFAFDKQKQJLFGSDVDRTQWRFRFAGNLASG	120	
Db	61	IPKEGVLSFWRGNNLANVIRYEPFQALNFAFDKQKQJLFGSDVDHTQWRFRFAGNLASG	120	
Oy	121	GAGATSLCEFYPLDPARTRLADYKGAKEEERFGLDCLVYKSDGIKELYOGFNVS	180	
Db	121	GAGATSLCEFYPLDPARTRLADYKGSCTEERFGLDCLVYKSDGIRGLYOGFSVS	180	
Oy	181	VOGIIITRAAYFGIYDTAKGMLPDERKNHIVISWMIAGTVTAAGLITSEPTVRRMM	240	
Db	181	VOGIIITRAAYFGVYDTAKGMLPDERKNHIVISWMIAGTVTAAGVASTPEFTVRRMM	240	
Oy	241	OSGRGKTDIMYGTLLDCKWRTIARDGGAKEFGAMSNVIRGGAAPVLVLYEIK	296	
Db	241	OSGRGADIMYGTGVYDCKWKITFRDGGGAKEFGAMSNVIRGGAAPVLVLYEIK	296	

RESULT 5	
AAM39641	
ID	AAM39641 standard; Protein: 298 AA.
XX	
AC	AAM39641;
XX	
DT	22-OCT-2001 (first entry)
XX	
DE	Human polypeptide SEQ ID NO 2786.
XX	
KW	Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW	peripheral nervous system; neuropathy; central nervous system; CNS;
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW	chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW	leukemia.
XX	
OS	Homo sapiens.
XX	
PN	MO200153312-A1.
XX	
PD	26-JUL-2001.
XX	
PF	26-DEC-2000; 2000MO-US34263.
XX	
PR	21-JAN-2000; 2000US-0488725.
PR	25-APR-2000; 2000US-0552317.
PR	09-JUL-2000; 2000US-0598042.
PR	19-JUL-2000; 2000US-0620312.
PR	03-AUG-2000; 2000US-0653450.
PR	14-SEP-2000; 2000US-0662181.
PR	19-OCT-2000; 2000US-0693036.
PR	29-NOV-2000; 2000US-0727344.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX	
PI	Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX	
DR	WPI: 2001-442253/47.
DR	N-PSDB: AAI58797.
XX	
PT	Novel nucleic acids and polypeptides, useful for treating disorders
PT	such as central nervous system injuries -
XX	
PS	Example 4; SEQ ID NO 2786; 10078bp; English.
XX	

xx	The invention relates to human nucleic acids (AA157798-AA161369) and			
cc	the encoded polypeptides (AAM8642-AAM42213) with neurotrophic,			
cc	immunosuppressant and cytostatic activity. The polynucleotides are useful			
cc	in gene therapy. A composition containing a polypeptide or polynucleotide			
cc	of the invention may be used to treat diseases of the peripheral nervous			
cc	system, such as peripheral nervous injuries, peripheral neuropathy and			
cc	localised neuropathies and central nervous system diseases, such as			
cc	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic			
cc	lateral sclerosis and Shy-Drager Syndrome. Other uses include the			
cc	utilisation of the activities such as: immune system suppression,			
cc	activation/inhibit activity, chemotactic/chemokinetic activity, hemostatic			
cc	and thrombolytic activity, cancer diagnosis and therapy, drug screening,			
cc	assays for receptor activity, arthritis and inflammation, leukaemias and			
cc	C.N.S. disorders.			
cc	Note: The sequence data for this patent did not form part of the printed			
xx	specification.			
cc				
xx				
Sequence	298 AA:			
Query Match	94.0%:	Score 1454:	DB 22:	Length 298:
Best Local Similarity	92.6%:	Pred. NO. 1.5e-144:		
Matches 274:	Conservative 13:	Mismatches 9:	Indels 0:	Gaps 0:

OY		1	MMDALSPFKDDPLAGGVAAAIKSTAVAPLERVKLLLOVOHASKOTADPOVGGIIDCYVR	60
			: : : : : : : : : : : : : : : : : :	
			: : : : : : : : : : : : : : : : : :	
Dd		1	MEEQATISEFKEKDPLAGGIAAISKTAVAPERLKKLLLOVOHASKOIADAOVYGIVDCIVR	60
OY		61	IPEEDEVLSFWMGNLANVIREFPTQALNEAFEDKYKQTFLFGVDRTQTFWRFEAGNLASG	120
			: : : : : : : : : : : : : : : : :	
Dd		61	IPKEGVSLSEFMWGNLANVIREFPTQALNFAFDXTKQIFLGSDKHHTQGWRFAFNLASG	120
OY		121	GAGATSILCEFYPLDPARTRLAADVGAKAEREERGLGDCLVKIKYSDGIGLYGFNVVS	180
			: : : : : : : : : : : : : : : :	
Dd		121	GAGATSILCEFYPLDFPARTRLAADVGKSGTEREFRLGDCLVKITKSOGIRGLYOGFSVS	180
OY		181	VGGIIITTYRAAYNGVIDTAKGMLPDEKNTHIVISMMIAOQTVTAAGVSYFPDTRRRMM	240
			: : : : : : : : : : : : : : : :	
Dd		181	VGGIIITTYRAAYNGVIDTAKGMLPDERKNTIHIVSMMIAOQTVTAAGVSYFPDTRRRMM	240
OY		241	OSGRKGTDIMYGTLDPCMKRIARDEGSKAFFKGAMSNVLRGGAFFVLVYLDEIKK	296
			: : : : : : : : : : : : : : : :	
Dd		241	QSQRKGADIMYGTIVDCKMRKIFREDEGKAFFKGANSNVLRGGAFFVLVYLDLKK	296
RESULT	6			
AAU01200				
ID	AAU01200 standard; Protein; 298 AA.			
XX	AAU01200;			
AC				
XX				
DT	07-SEP-2001 (first entry)			
XX				
DE	Human adenine nucleotide translocator-3 (ANT-3) protein.			
XX				
KW	Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;			
KW	mitochondrial permeability transition pore component; cell survival;			
KW	mitochondrial core component; mitochondrial related disorder; cancer;			
KW	Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.			
XX				
OS	Homo sapiens.			
XX				
PN	WO200132876-AZ.			
XX				
PD	10-MAY-2001.			
PF				
XX	03-NOV-2000; 200OWO-US30535.			
PR	03-NOV-1999; 99US-0434354.			
XX				
PA	(MITO-) MITOKOR.			
PI	Murphy AN, Cleveland W, Wiley SE, Andreyev AY, Ffrench LF,			

XX 22-OCT-2001 (first entry)
DT Human polypeptide SEQ ID NO 6358.
DE
XX
KW Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
XX N-PSDB: AAI60583.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries -
XX
XX Example 2: SEQ ID NO 6358; 10078bp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and
XX the encoded polypeptides (AA38642-AA42213) with noctropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: Immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokine activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemia and
XX C.N.S disorders.
XX Note: The sequence data for this patent did not form part of the printed
XX specification.
XX
XX Sequence 323 AA;
SQ
Query Match 94.0%; Score 1454; DB 22; Length 323;
Best Local Similarity 92.6%; Pred. No. 1,7e-144;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 1 MTDALSPAKDFLAGVAAIAISKTAIVAPIERVKLLLOVQHASKOITADKQYKGIIDCVR 60
DB MTEOAIISFAKDFLAGVAAIAISKTAIVAPIERVKLLLOVQHASKOIADKQYKGIIDCVR 85
QY 61 IPKQOVLSPFRGNLANVIRPEPQALNFARFKDKYKQIFLGVDVKRQGFWRFFAGNLASG 120
DB 86 IPKQOVLSPFRGNLANVIRPEPQALNFARFKDKYKQIFLGVDVKRQGFWRFFAGNLASG 145

QY 121 GAAGATSLCFYVPLDFARTRLADVGKAGAREERFGLGDLVTKIKYSPGICKLYQGFNV 180
DB 146 GAAGATSLCFYVPLDFARTRLADVGKAGAREERFGLGDLVTKIKYSPGICKLYQGFNV 205
QY 181 VOGIIIRAAVFGIYDFAKGLPDPKNTHTIVISWMIADTVAVAGLTSYPTVRRMM 240
DB 206 VOGIIIRAAVFGIYDFAKGLPDPKNTHTIVISWMIADTVAVAGLTSYPTVRRMM 265
QY 241 QSGRKGDTIMYGTGTLDCWRKIAARDEGKAFKAGMSNVLROMGAFVLYLDELKK 296
DB 266 QSGRKGADIMYGTGTLDCWRKIAARDEGKAFKAGMSNVLROMGAFVLYLDELKK 321
RESULT 9
ABG15423
ID ABG15423 standard; Protein: 325 AA.
XX
XX ABG15423;
XX
XX 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #15414.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
XX N-PSDB: AAS79610.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 20; SEQ ID NO 45782; 103bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 325 AA:
 SO Query Match 91.6%; Score 1417; DB 22; Length 325;
 Best Local Similarity 92.7%; Pred. No. 1.4e-140;
 Matches 280; Conservative 3; Mismatches 15; Indels 4; Gaps 3;

OY 1 MTDAAISFPAKDFLAGVAAAIKSTAVAPIERVKLLLOVQHASQITADKQYKGIIDCVVR 60
 |||||
 DB 24 MTDAAVSFAKDFLAGVAAAIKSTAVAPIERVKLLLOVQHASQITADKQYKGIIDCVVR 83
 OY 61 IPKEQEVLSFWRGNLAVIRYPTQALNFAFKDKYKQIFLGVDKRTQEFWRYPAGNLASG 120
 |||||
 DB 84 IPKEQEVLSFWRGNLAVIRYPTQALNFAFKDKYKQIFLGVDKRTQEFWRYPARNLASG 143
 OY 121 GAAGATSLCFVYPLDFARTRLAADVCKAGAEERFGLDCLVKIYKSDGIKGLYQGFNVS 180
 |||||
 DB 144 GAAGATSLCFVYPLDFARTRLAADVCKAGAEERFGLDCLVKIYKSDGIKGLYQGFNVS 203
 OY 181 VOGIITRYRAAYFGIYDTAKGMLDPKNTHTIVISMIAQTVHCCPGXLPFPDTRSVRN 237
 |||||
 DB 204 VOGIITRYRAAYFGIYDTAKGMLDPKNTHTIVISMIAQTVHCCPGXLPFPDTRSVRN 263
 OY 238 MMQSGRKGTIDIMYTGTLDCMRKIADEGKAFKFGKAMSVNLKMGCAFVLVLYD-EIKK 296
 |||||
 DB 264 EXMQSGRKGTIDIMYTGTLDCMRKIADEGKAFKFGKAMSVNLKMGCAFVLVLYEKKSK 323
 OY 297 YT 298
 ||
 DB 324 YT 325

RESULT 10
 AAM61169
 ID AAM61169 standard; Protein: 298 AA.
 XX
 AC AAM61169;
 XX
 DT 28-SEP-1998 (first entry)
 XX
 DE Anti protein.
 XX
 XX Anti: Adenine nucleotide translocator: cloning; screening;
 KW DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation;
 KW probe: OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;
 KW hyperlactic acidosis; degenerative muscle disease.
 KW lactic acidosis; degenerative muscle disease.
 XX
 OS Mus sp.
 XX
 PN WO9819714-A1.
 XX
 PD 14-MAY-1998.
 XX
 PF 31-OCT-1997; 97WO-US19882.
 XX
 PR 01-NOV-1996; 96US-0030017.
 XX
 PA (UYEM-) UNIV EMORY.
 XX
 PI Graham BC, Macgregor GR, Wallace DC;
 XX
 DR WPI: 1998-286608/25.
 DR N-PSDB: AAV36479.
 XX
 XX Mice lacking heart-muscle adenine nucleotide translocator protein -
 PT useful as model for mitochondrial myopathy and hyperlactic
 PT cardiomyopathy in animals and to test therapeutic compositions or
 PT gene therapies
 XX
 PS Disclosure: Page 39-40; 61pp; English.
 XX
 CC The present sequence is the mouse Anti protein, the cDNA producing this

CC polypeptide is cloned by screening a mouse heart cDNA library with the
 CC human Anti cDNA as a probe. The Anti cDNA sequence was determined by DNA
 CC Tag dideoxy terminator cycle sequencing. The Anti protein is encoded by
 CC the Anti locus, a nuclear gene on chromosome 8. This protein is required
 CC in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP
 CC which can then be converted into ATP. An Anti homozygous mutant would
 CC thus be defective in OXPHOS which results in disease in oxidative
 CC metabolism dependent tissues. This mouse Anti homozygous mutant can be
 CC used as a model system for fascioscapular humeral muscular dystrophy,
 CC hyperlactic acidosis, myopathy, lactic acidosis, etc. These model
 CC systems can be used to test possible therapeutic compounds which
 CC increase/mediate ATP and ADP exchange across the mitochondrial membrane
 CC independent of Anti.
 XX
 SO Sequence 298 AA:
 Query Match 91.2%; Score 1411; DB 19; Length 298;
 Best Local Similarity 89.2%; Pred. No. 5.2e-140;
 Matches 265; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

OY 1 MTDAAISFPAKDFLAGVAAAIKSTAVAPIERVKLLLOVQHASQITADKQYKGIIDCVVR 60
 |||||
 DB 1 MTDAAVSFPAKDFLAGVAAAIKSTAVAPIERVKLLLOVQHASQITADKQYKGIIDCVVR 60
 OY 61 IPKEQEVLSFWRGNLAVIRYPTQALNFAFKDKYKQIFLGVDKRTQEFWRYPAGNLASG 120
 |||||
 DB 61 IPKEQEVLSFWRGNLAVIRYPTQALNFAFKDKYKQIFLGVDKRTQEFWRYPAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLAADVCKAGAEERFGLDCLVKIYKSDGIKGLYQGFNVS 180
 |||||
 DB 121 GAAGATSLCFVYPLDFARTRLAADVCKAGAEERFGLDCLVKIYKSDGIKGLYQGFNVS 180
 OY 181 VOGIITRYRAAYFGIYDTAKGMLDPKNTHTIVISMIAQTVHCCPGXLPFPDTRSVRN 240
 |||||
 DB 181 VOGIITRYRAAYFGIYDTAKGMLDPKNTHTIVISMIAQTVHCCPGXLPFPDTRSVRN 240
 OY 241 QSGRKGTIDIMYTGTLDCMRKIADEGKAFKFGKAMSVNLKMGCAFVLVLYDEIKKY 297
 |||||
 DB 241 QSGRKGTIDIMYTGTLDCMRKIADEGKAFKFGKAMSVNLKMGCAFVLVLYDEIKKY 297

RESULT 11
 AAY71031
 ID AAY71031 standard; Protein: 297 AA.
 XX
 AC AAY71031;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Human adenine nucleotide translocator ANTI.
 XX
 XX Human:
 KW Human: adenine nucleotide translocator; ANTI; mitochondria; ADP; ATP;
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; nocturnal;
 KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
 KW antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KW diabetes; Leber's hereditary optic neuropathy; stroke; MIDD;
 KW mitochondrial encephalopathy; lactic acidosis; schizophrenia; MELAS;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200026370-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 03-NOV-1999; 99WO-US25883.
 XX
 PR 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 XX

PA (MITO-) MITOKOR.
XX
PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI Ghosh SS;
XX
DR WPI: 2000-365619/31.
DR N-PSDB: AAD00519.
XX
PT Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease -
XX
PS Claim 44: Page 172; 175pp; English.
XX
CC The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MTD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT1 from human brain.
XX
SQ Sequence 297 AA;
XX
Query Match 89.9%; Score 1391.5; DB 21; Length 297;
Best Local Similarity 88.6%; Pred. No. 5.9e-138;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
XX
QY 1 MTDALSFAPKDFLAGVAAATSKTAVAPIERVKLLQVHASKQITADKQYKGIIDCVVR 60
Db 1 MGDHAWSLFKDPLAGAVAAVSKTAVAPIERVKLLQVHASKQISAKQYKGIIDCVVR 60
QY 61 IPKDEVSFWKRGNLANTIRFPTQALNFAFKDKYKQIFLGGVDKRTQFMYFFAGNLASG 120
Db 61 IPKDEGFLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGGVDKRTQFMYFFAGNLASG 120
QY 121 GAAGATSLCFYYPDLPARTRLAADYGKAGAEFRFGLDCLVKTIYKSGITGLYOGFNVS 180
Db 121 GAAGATSLCFYYPDLPARTRLAADYGR-AQREFHGLDCLTIKFSGLGLYOGFNVS 179
QY 181 VOGIITIRAAVFGIYDTAKGMLPDPKNTNHIYSWMIAGTVAAGLTSYPPDYRRRMM 240
Db 180 VOGIITIRAAVFGIYDTAKGMLPDPKNTNHIYSWMIAGTVAAGLTSYPPDYRRRMM 239
QY 241 QSGRKGTDIMTGTGIDCKRKTARDEGKAFKAGMSNVLRMGCAFVLYLDEIKKY 297
Db 240 QSGRKGADIMTGTVDCKRIAKDEGAKAFKAGMSNVLRMGCAFVLYLDEIKKY 296
XX
RESULT 12
AAU01198
ID AAU01198 standard; Protein: 297 AA.
XX
AC AAU01198;
XX
DE 07-SEP-2001 (first entry)
XX
XX Human adenine nucleotide translocator-1 (ANT-1) protein.
XX
XX Human adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
KW mitochondrial permeability transition pore component; cell survival;
KW mitochondrial core component; mitochondrial related disorder; cancer;
KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

XX
OS Homo sapiens.
XX
PN WO200132876-A2.
XX
XX 10-MAY-2001.
PD
XX
XX 03-NOV-2000; 2000WO-US30535.
XX
XX 03-NOV-1999; 99US-0434354.
XX
XX (MITO-) MITOKOR.
PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
PI Velicelcib G, Davis RE;
XX
XX WPI: 2001-291054/30.
DR N-PSDB: AAS05901.
XX
DR New nucleic acid expression constructs, useful for screening for agents
PT that alter mitochondrial permeability transition (MPT), comprises
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
PT fused to energy transfer molecule -
XX
XX Disclosure: Fig 2; 186pp; English.
XX
CC The present sequence represents human adenine nucleotide translocator-1
CC (ANT-1) protein. ANT proteins are mitochondrial permeability
CC transition (MTP) pore components responsible for mediating transport
CC of ADP across the mitochondrial inner membrane. ANT proteins interact
CC with other mitochondrial core components e.g. cyclophilins to
CC regulate MPT. The present invention relates to a novel nucleic acid
CC expression construct comprising a promoter operably linked to a
CC polynucleotide encoding a mitochondrial pore component polypeptide
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC (e.g. green fluorescent protein (GFP) or a FLAHS sequence). The novel
CC expression construct can alter mitochondrial membrane permeability
CC transition and/or alter the interaction between mitochondrial core
CC components. The methods are useful for screening for agents that alter
CC MPT and/or cell survival. These agents are useful for the prevention or
CC treatment of diseases associated with altered mitochondrial function or
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC mitochondrial encephalopathy, lactic acidosis, stroke,
CC hyperproliferative disorders e.g. cancer, and deafness.
XX
SQ Sequence 297 AA;
XX
Query Match 89.9%; Score 1391.5; DB 22; Length 297;
Best Local Similarity 88.6%; Pred. No. 5.9e-138;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
XX
QY 1 MTDALSFAPKDFLAGVAAATSKTAVAPIERVKLLQVHASKQITADKQYKGIIDCVVR 60
Db 1 MGDHAWSLFKDPLAGAVAAVSKTAVAPIERVKLLQVHASKQISAKQYKGIIDCVVR 60
QY 61 IPKDEVSFWKRGNLANTIRFPTQALNFAFKDKYKQIFLGGVDKRTQFMYFFAGNLASG 120
Db 61 IPKDEGFLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGGVDKRTQFMYFFAGNLASG 120
QY 121 GAAGATSLCFYYPDLPARTRLAADYGKAGAEFRFGLDCLVKTIYKSGITGLYOGFNVS 180
Db 121 GAAGATSLCFYYPDLPARTRLAADYGR-AQREFHGLDCLTIKFSGLGLYOGFNVS 179
QY 181 VOGIITIRAAVFGIYDTAKGMLPDPKNTNHIYSWMIAGTVAAGLTSYPPDYRRRMM 240
Db 180 VOGIITIRAAVFGIYDTAKGMLPDPKNTNHIYSWMIAGTVAAGLTSYPPDYRRRMM 239
QY 241 QSGRKGTDIMTGTGIDCKRKTARDEGKAFKAGMSNVLRMGCAFVLYLDEIKKY 297
Db 240 QSGRKGADIMTGTVDCKRIAKDEGAKAFKAGMSNVLRMGCAFVLYLDEIKKY 296

RESULT 13
AAU10378
ID AAU10378 standard; Protein: 297 AA.
XX
AC AAU10378;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human adenine nucleotide translocator 1 (ANT1).
XX
KW Human: adenine nucleotide translocator; ANT;
KW mitochondrial matrix protein.
XX
OS Homo sapiens.
XX
PN MO200185944-A2.
XX
PD 15-NOV-2001.
XX
PF 11-MAY-2001; 2001WO-US15416.
XX
PR 11-MAY-2000; 2000US-0569327.
XX
PA (MITO-) MITOKOR.
XX
PI Anderson CM, Davis RE, Clevenger W, Willey SE, Miller SM, Szabo TR;
PI Ghosh SS, Moos WH, Pel Y, Carroll AK;
XX
DR WPI: 2002-055598/07.
DR N-PSDB: AAS16688.
XX
PT Novel recombinant expression construct for producing adenine nucleotide
PT translocator polypeptides, comprises a regulated promoter linked to
PT nucleic acid encoding the polypeptide
XX
PS Claim 44; Fig 2; 147pp; English.
XX
CC The invention relates to a recombinant expression construct (I)
CC comprising a regulated promoter operably linked to a nucleic acid
CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC proteins mediate the exchange of ATP synthesised in the mitochondrial
CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
CC culturing the host cell. (I) is also useful for targeting a polypeptide
CC of interest to a mitochondrial membrane, where ANT polypeptide is
CC expressed as a fusion protein with the polypeptide of interest.
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC useful for identifying an agent that binds to an ANT polypeptide. ANT
CC ligand is useful for determining the presence of an ANT polypeptide,
CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
CC ANT from a biological sample, where the ANT ligand is covalently or non-
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC useful for identifying an agent that interacts with an ANT polypeptide.
CC The present sequence represents the amino acid sequence of human ANT1.
XX
SQ Sequence 297 AA:
XX
Query Match 89.9%; Score 1391.5; DB 23; Length 297;
Best Local Similarity 88.6%; Pred. No. 5.9e-138;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
OY 1 MTEAALSFADFLAGVAAAIKTAAPVIRVKLLLOVQASHKOITFADKOYKGIIDCVR 60
DB 1 MGHANSLKDFLAGVAAVAASKTAAVPIRVKLLLOVQASHKOISAEKYGKGIIDCVR 60
OY 61 IPKEDEVLSTWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFRAGNLASG 120
DB 61 IPKEDEVLSTWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFRAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTLADVKGAGAREFERGIDGLVITKSDGIRKGLYOGNVS 180
DB 121 GAAGATSLCFVYPLDFARTLADVGNR-AOREFHGIGDICTIKIFKSDGLRGLYOGNVS 179

OY 181 VOGIIIRAAVFGIYDTAKGMLPDPKNTHIVSMIAQTVAAVAGLSTPFDVRRMM 240
DB 180 VOGIIIRAAVFGVYDTAKGMLPDPKNTHIVSMIAQSTVAAGLSTPFDVRRMM 239
OY 241 QSGRRKGTIDIMYGTGLDCMRKRIANDEGKAFFKGAWSNVLKMGCAFVLVYDEIKKY 297
DB 240 QSGRRKGTIDIMYGTGLDCMRKRIANDEGKAFFKGAWSNVLKMGCAFVLVYDEIKKY 296
RESULT 14
ABG27056
ID ABG27056 standard; Protein: 263 AA.
XX
AC ABG27056;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #27047.
XX
KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN MO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB: AAS91243.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 20; SEQ ID No 57415; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 263 AA:
XX
Query Match 87.0%; Score 1346; DB 22; Length 263;
Best Local Similarity 99.2%; Pred. No. 3.1e-133;

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:44:25 ; Search time 11.6797 Seconds

(without alignments)
750.705 Million cell updates/sec

Title: US-09-393-441-32

Perfect score: 1547

Sequence: 1 MTDALSFADFLAGVAA.....LRGGAFLVLYDEIKKYT 298

Scoring table:

BIOSUM62

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfilltest.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1411	91.2	298	US-08-961-871-10	Sequence 10, Appl
2	301	19.5	469	US-09-188-930-339	Sequence 339, App
3	274	17.7	291	US-09-501-558-2	Sequence 2, Appl
4	261.5	16.9	447	US-09-160-119-4	Sequence 4, Appl
5	261.5	16.9	674	US-09-160-119-2	Sequence 2, Appl
6	247	16.0	312	US-09-142-565-2	Sequence 2, Appl
7	244.5	15.8	311	US-08-775-009-33	Sequence 33, Appl
8	239.5	15.5	309	US-08-518-878B-51	Sequence 51, Appl
9	239.5	15.5	309	US-08-807-861A-51	Sequence 51, Appl
10	239.5	15.5	309	US-08-470-868A-51	Sequence 51, Appl
11	239.5	15.5	309	US-09-210-681-51	Sequence 51, Appl
12	239.5	15.5	309	US-08-946-719A-51	Sequence 56, Appl
13	236.5	15.3	299	US-08-518-878B-56	Sequence 56, Appl
14	236.5	15.3	299	US-08-470-868A-56	Sequence 32, Appl
15	232.5	15.0	311	US-08-775-009-32	Sequence 32, Appl
16	230.5	14.9	320	US-08-933-750C-12	Sequence 12, Appl
17	230.5	14.9	320	US-09-234-613-12	Sequence 12, Appl
18	227	14.7	308	US-08-937-466-2	Sequence 2, Appl
19	227	14.7	308	US-09-172-528-2	Sequence 2, Appl
20	227	14.7	308	US-09-318-199-2	Sequence 2, Appl
21	227	14.7	308	US-09-503-579-2	Sequence 2, Appl
22	223	14.4	432	US-08-937-466-4	Sequence 4, Appl
23	223	14.4	432	US-09-172-528-4	Sequence 4, Appl
24	223	14.4	432	US-08-946-719A-56	Sequence 4, Appl
25	223	14.4	432	US-09-318-199-4	Sequence 4, Appl
26	219.5	14.2	293	US-09-503-579-4	Sequence 4, Appl
27	218.5	14.1	303	US-08-294-532B-36	Sequence 36, Appl

28	217.5	14.1	303	1	US-08-518-878B-37	Sequence 37, Appl
29	217.5	14.1	303	2	US-08-807-861A-37	Sequence 37, Appl
30	217.5	14.1	303	3	US-08-470-868A-37	Sequence 37, Appl
31	217.5	14.1	303	3	US-09-210-681-37	Sequence 37, Appl
32	217.5	14.1	303	3	US-08-946-719A-37	Sequence 37, Appl
33	191	12.3	328	4	US-09-068-140A-15	Sequence 15, Appl
34	190.5	12.3	256	2	US-08-937-466-6	Sequence 6, Appl
35	190.5	12.3	256	2	US-09-172-528-6	Sequence 6, Appl
36	190.5	12.3	256	3	US-09-318-199-6	Sequence 6, Appl
37	190.5	12.3	256	4	US-09-503-579-6	Sequence 6, Appl
38	189	12.2	306	5	PCT-US94-09799-1	Sequence 1, Appl
39	187.5	12.1	307	2	US-08-807-861A-56	Sequence 56, Appl
40	187.5	12.1	307	3	US-09-210-681-56	Sequence 56, Appl
41	187.5	12.1	307	3	US-08-946-719A-56	Sequence 56, Appl
42	187	12.1	351	2	US-08-933-750C-19	Sequence 19, Appl
43	187	12.1	351	4	US-09-234-613-19	Sequence 19, Appl
44	181	11.7	289	4	US-09-068-140A-10	Sequence 10, Appl
45	173.5	11.2	312	4	US-09-188-930-142	Sequence 142, App

ALIGNMENTS

RESULT 1
US-08-961-871-10
Sequence 10, Application US/08961871
Patent No. 6013858
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-871-10
Query Match 91.2%, Score 1411, DB 3, Length 298;
Best Local Similarity 89.2%, Pred. No. 2.8e-154;
Matches 265; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
OY 1 MTDALSFADFLAGVAAISKAVAPIERVKLLQVHMSKQITADKQYKGIIDCVVR 60

```
Db      1 MGQALSPFKDLAGGIAAASVTAAVPIERVLLLOVHASKQIAEKQKGIIDCV 60
Qy      61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKOIFLGVDKRTQFWRYPAGNLASG 120
Db      61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKOIFLGVDKRTQFWRYPAGNLASG 120
Qy      121 GAAGATSLCFVYPLDFAFRLADVAGAKAEERERGLGDLVKYKSDGKGLYOGFNVS 180
Db      121 GAAGATSLCFVYPLDFAFRLADVAGKSSQREFNGISGDLTKIFKSDGLKGLYOGFNVS 180
Qy      181 VOGIIIRAAVFGIYDTAGMLPDPKNTHTVISMIAQVYTAAGITSPFDVRRRMM 240
Db      181 VOGIIIRAAVFGIYDTAGMLPDPKNTHTVISMIAQSVTAAGLVSPFDVRRRMM 240
Qy      241 QSGRKGTDIMYTGTLDCWKRIAREGKAFFKGAWSNVLRGMGAFVLYDEIKKY 297
Db      241 QSGRKGADIMYTGTLDCWKRIAREGKAFFKGAWSNVLRGMGAFVLYLYDEIKKY 297
```

RESULT 2

US-09-188-930-339

Sequence 339, Application US/09188930A

Patent No. 6150502

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Strachan, Lorna

APPLICANT: Sleeman, Matthew

APPLICANT: Onrust, Rene

APPLICANT: Murlson, James Greg

TITLE OF INVENTION: Compositions Isolated From Skin Cells

FILE REFERENCE: 11000.1011c1

CURRENT FILING DATE: 1998-11-09

NUMBER OF SEQ ID NOS: 348

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 339

LENGTH: 469

TYPE: PRT

ORGANISM: Mouse

US-09-188-930-339

Query Match 19.5%; Score 301; DB 4; Length 469;

Best Local Similarity 28.4%; Pred. No. 5e-26;

Matches 86; Conservative 62; Mismatches 109; Indels 46; Gaps 12;

```
Qy      10 KDLACGVAATAISKTAIVAPIERVKLLLOVHASKQITADKQYKGIIDCV----RIPKEQ 65
Db      188 RHLVAGGGAASRTCTAPLDRKVLMOV--HASRSNNM-----CIVGFTQMIREG 237
Qy      66 EVLSFWRGNLANVIRYPTQALNFAFKDKYKOIFLGVDKRTQFWRYPAGNLASGGAAG 125
Db      238 GAKSLMRGNINVLKTAIPESAIKFMAYEQMKR--LVGSOET---LRHERLVAGSLAGA 292
Qy      126 TSLCFVYPLDFAFRLADVAGAKAEERERGLGDLVKYKSDGKGLYOGFNVSVOGII 185
Db      293 IQOSSYIPMEVLTIRMA--LRKTG---QYSGMDCARILAKGVAAAFKGYIPNMLGIT 347
Qy      186 IYRAAFYGYIDRAKGLPDPKNTHTVISMIAQVYTAAG--LTSFPDPT 233
Db      348 PLAGIDLAYEYL-----KNTWLDORYVNSADPGVFLVLLACGTISSYCGQLASTYPLAL 400
Qy      234 VRRMMQSGRKGTDMYTGTLDCWKRIAREGKAFFKGAWSNVLRGMGAFV--LVLYD 292
Db      401 VETRMQQAQSIQAPRYTMSL--FKQILRTBQAGLILYGLAPNFKVLPANISIVYIE 458
Qy      293 EIK 295
Db      459 NLK 461
```

*RESULT 3

```
US-09-501-558-2
Sequence 2, Application US/09501558
Patent No. 6403784
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Mathur, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and
FILE REFERENCE: LEX-0012-USA
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 291
TYPE: PRT
ORGANISM: Homo sapiens
US-09-501-558-2
```

Query Match 17.7%; Score 274; DB 4; Length 291;

Best Local Similarity 27.8%; Pred. No. 3.1e-23;

Matches 85; Conservative 55; Mismatches 134; Indels 32; Gaps 9;

```
Qy      4 AALSPFKDLAGGVAATAISKTAIVAPIERVKLLLOVHASKQITADKQYKGIIDCV 58
Db      2 SALNM--KRPVYGGSLATFACGFFPIDLTKRTRQIGQGNDAKKFKI-----HYRGLMHL 56
Qy      59 VRIPEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKOIFLGVDKRTQFWRYPAGNL 118
Db      57 VRIGREGKALYSGIAPMLRQASYGITKIGYOSLKRFLTERPDEP-----LPINVI 111
Qy      119 SGGAATSLCFVYPLDFAFRLADVAGAKAEERERGLGDLVKYKSDGKGLYOGFN 178
Db      112 CGILSGVISSTIANPYDTVKIRMQAOSNTIQ-----GIGNFMNLYQOEGTRGLMKVS 166
Qy      179 VSVQGIIRAAVFGIYDTAK-----GMLPDPKNTHTVISMIAQVYTAAGLTSYPPD 232
Db      167 LTAQRAIYVGVYELPYDTTKHLISGLMGDVTYTHLSF-----TCLAGLANSNPD 222
Qy      233 TVRRMMQSG--RKGTDMYTGTLDCWKRIAREGKAFFKGAWSNVLR--GMGAFVLYL 290
Db      223 VVETRMQNRVLRDGRGSGYTGTLDCLOTWKNEGFALYKGFPMWLRIGPWNITFEVT 282
Qy      291 YDEIK 296
Db      283 YEQLK 288
```

RESULT 4

US-09-160-119-4

Sequence 4, Application US/09160119A

Patent No. 6316219

GENERAL INFORMATION:

APPLICANT: KRIEF, STEPHANE

APPLICANT: SOUCHEP, MICHEL

APPLICANT: BRIL, ANTOINE

TITLE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GH-30965

CURRENT APPLICATION NUMBER: US/09/160,119A

CURRENT FILING DATE: 1998-09-24

EARLIER APPLICATION NUMBER: EP 97402511.6

EARLIER FILING DATE: 1997-10-23

EARLIER APPLICATION NUMBER: EP 98401655.0

EARLIER FILING DATE: 1998-07-02

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4

LENGTH: 447

TYPE: PRT

ORGANISM: HOMO SAPIENS

US-09-160-119-4

[illegible]

```

RESULT 5
US-09-160-119-2
: Sequence 2, Application US/09160119A
: Patent No. 6316219
: GENERAL INFORMATION:
: APPLICANT: KRIEF, STEPHANE
: APPLICANT: SOUCHEP, MICHEL
: APPLICANT: BRIL, ANTOINE
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GH-30985
: CURRENT APPLICATION NUMBER: US/09/160.119A
: CURRENT FILING DATE: 1998-09-24
: EARLIER APPLICATION NUMBER: EP 97402511.6
: EARLIER FILING DATE: 1997-10-23
: EARLIER APPLICATION NUMBER: EP 98401655.0
: EARLIER FILING DATE: 1998-07-02
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 674
:
: TYPE: PR1
: ORGANISM: HOMO SAPIENS
: US-09-160-119-2

```

[illegible]

```

RESULT 6
US-09-142-565-2
: Sequence 2, Application US/09142565A
: Patent No. 6187560
: GENERAL INFORMATION:
: APPLICANT: Lee James Beeley
: APPLICANT: Kelly Paine
: APPLICANT: Robert James
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GH-30002
: CURRENT APPLICATION NUMBER: US/09/142,565A
: CURRENT FILING DATE: 1999-06-30
: EARLIER APPLICATION NUMBER: 9704551.2
: EARLIER FILING DATE: 1997-03-05
: EARLIER APPLICATION NUMBER: 9705614.7
: EARLIER FILING DATE: 1997-03-18
: EARLIER APPLICATION NUMBER: 97305305.1
: EARLIER FILING DATE: 1997-07-16
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 312
: TYPE: PRT
: ORGANISM: HOMO SAPIEN
US-09-142-565-2

```

Query	March	16.0%	Score	247	DB	4	Length	312	
Best	Local Similarity	24.8%	Pred.	0.4.5e-20					
Matches	76	Conservative	56	Mismatches	149	Indels	26	Gaps	8
Db									
Qy	2	TDAAISFAKDFLAGGVAANAISKTAAPIERVVKLLLOVOHASKOITADK--QYKGIIDCVV	59						
		: : : : : : : : : : : : : : : : : :							
Db	7	SDVPPTMAVKFLGAGTACGADLVLPFDPTAKVRQIOGEMNAVQTRALRYQIRGVIGTLL	66						
		: : : : : : : : : : : : : : : : : :							
Qy	60	RIPKQEVLSFWRGILANVIRYEPFOALNFAFKDKYKQIFL--GGYDKRTQFMYRFAGNLA	118						
		: : : : : : : : : : : : : : : : : :							
Db	67	TWVFREGPCSPNGVLVAGLOROMSFASIRIGLIDYSKQYVTFPKGADNSSLTTRILA----	122						
		: : : : : : : : : : : : : : : : : :							
Qy	119	SGGAGARSLCEVYVYLDLDFARTRLADV--GKAGAEERFEGLDCLVKKIKSGIKGLYOG	176						
		: : : : : : : : : : : : : : : : : :							
Db	123	-GCTTGAANAIVTCAOPLTDVVKVRFQASIHLPSPRSDDKYSGTMDAVRTIAREGVRQLMG	181						
		: : : : : : : : : : : : : : : : : :							
Qy	177	FNVSVOGILITRAAYFGIYDTAK-----GMLPDDEKNTHIVISMIAQVTAAGLTSP	230						
		: : : : : : : : : : : : : : : : : :							
Db	182	TLPNTMRNAIVNCAEVYITDILKEKLDYHLTLDTNFPCHFVAFAGFGFCATVYAS----P	237						
		: : : : : : : : : : : : : : : : : :							
Qy	231	FDTVRRMMMSGKRGKTDIMTGTGLDCWRKRIARDEGKAFFKGAMSNVLR--GMGGAFLVY	289						
		: : : : : : : : : : : : : : : : : :							
Db	238	VDVVKTRVM-----NSPQGYRPSLPDCMKIKMAQEGPFTAFYKGFPPSLRLDSMNVMV	292						
		: : : : : : : : : : : : : : : : : :							
Qy	290	LYDEIK	296						
		: : : :							
Db	293	TYEQLR	299						

```

1  RESULT 7
2  US-08-775-009-33
3  : Sequence 33, Application US/0875009
4  : Patent No. 5935783
5  :
6  : GENERAL INFORMATION:
7  :
8  : APPLICANT: Gong, Wellong
9  : APPLICANT: Emanuel, Beverly S.
10 : APPLICANT: Budarf, Marcia L.
11 : APPLICANT: Roe, Bruce
12 :
13 : TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digestive and
14 : TITLE OF INVENTION: Velloocardiofacial Syndrome Minimal Critical Region
15 :
16 : NUMBER OF SEQUENCES: 45
17 :
18 : CORRESPONDENCE ADDRESS:
19 :
20 : ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
21 : ADDRESSEE: No. 5935783rls, LLP
22 :
23 : STREET: One Liberty Place - 46th Floor

```


APPLICATION NUMBER: US/08/807,861A
FILING DATE: 26-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELETYPE: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-807-861A-51

Query Match 15.5%; Score 239.5; DB 2; Length 309;
Best Local Similarity 23.5%; Pred. No. 3.2e-19;
Matches 72; Conservative 58; Mismatches 149; Indels 27; Gaps 8;

QY 2 TDAALSFADKDLGAGVAAAIKSTAVAPIERVKLLQVOHASK---QITADKQYKGIIDCV 58
DB 7 TDVPTATVAVKFLGAGTACIADLITFPLDTAKVRLQIGESGCPVRAVSQYRKVMGTI 66
QY 59 VRIRKDEVLSEFMRGNLANVIRYPTQALNFAFKDKYQIFLGVDKRTCFMRRFAGNLA 118
DB 67 LTMVTEGPRSLYNGLVAGLQROMSFASVRIGLDVSKQFYTKGSEHAS-----IGSRL 121
QY 119 SGGAAGATSLCFVYPLDPAFRTRLADVGKAGAREFRGLGCLVITYSDGIKGLYGFN 178
DB 122 AGSTTGALAAVAAOPTDVVKYRFQAQ-ARAGGRRYQSTVNAKYRTIAREEGFRGLMKGT 180
QY 179 VSVGGIITRYAAVFGIYDTAK-----GMLPDPKNTHTIVISMIAQYTAAGLTSYFPD 232
DB 181 PNVARNAIVNCAELVLYLIDALLKANIMTDLPCHFTSAFGAFCCTVIAS-----PVD 236
QY 233 TVRRRMQMOS-GRKGTDMYGTGLDCMKRIARDEGKAFKFGANSNVLK-GMGAFVLYL 290
DB 237 VVKTRYMSALGQ-----YSSAGHCALTMLOKEGPRAFYKGFMPSLRLGSMNVVMFVT 290
QY 291 YDEIKK 296
DB 291 YEQLKR 296

RESULT 10
US-08-470-868A-51
Sequence 51, Application US/08470868A
Patent No. 5861485
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELETYPE: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-470-868A-51

Query Match 15.5%; Score 239.5; DB 2; Length 309;
Best Local Similarity 23.5%; Pred. No. 3.2e-19;
Matches 72; Conservative 58; Mismatches 149; Indels 27; Gaps 8;

QY 2 TDAALSFADKDLGAGVAAAIKSTAVAPIERVKLLQVOHASK---QITADKQYKGIIDCV 58
DB 7 TDVPTATVAVKFLGAGTACIADLITFPLDTAKVRLQIGESGCPVRAVSQYRKVMGTI 66
QY 59 VRIRKDEVLSEFMRGNLANVIRYPTQALNFAFKDKYQIFLGVDKRTCFMRRFAGNLA 118
DB 67 LTMVTEGPRSLYNGLVAGLQROMSFASVRIGLDVSKQFYTKGSEHAS-----IGSRL 121
QY 119 SGGAAGATSLCFVYPLDPAFRTRLADVGKAGAREFRGLGCLVITYSDGIKGLYGFN 178
DB 122 AGSTTGALAAVAAOPTDVVKYRFQAQ-ARAGGRRYQSTVNAKYRTIAREEGFRGLMKGT 180
QY 179 VSVGGIITRYAAVFGIYDTAK-----GMLPDPKNTHTIVISMIAQYTAAGLTSYFPD 232
DB 181 PNVARNAIVNCAELVLYLIDALLKANIMTDLPCHFTSAFGAFCCTVIAS-----PVD 236
QY 233 TVRRRMQMOS-GRKGTDMYGTGLDCMKRIARDEGKAFKFGANSNVLK-GMGAFVLYL 290
DB 237 VVKTRYMSALGQ-----YSSAGHCALTMLOKEGPRAFYKGFMPSLRLGSMNVVMFVT 290
QY 291 YDEIKK 296
DB 291 YEQLKR 296

RESULT 11
US-09-210-681-51
Sequence 51, Application US/09210681
Patent No. 6057109
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/518,878B
;; FILING DATE: 23-AUG-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7853-036
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 56:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 299 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;;
US-08-518-878B-56

Query Match 15.3%; Score 236.5; DB 1; Length 299;
Best local similarity 23.6%; Pred. No. 6.6e-19;
Matches 70; Conservative 57; Mismatches 142; Indels 27; Gaps 8;
;;
OY 12 FLAGVAAAIKSTAVAPIERVKLLQVOHASK---QITADQYGIIDCVIRIKDEVL 68
DB 7 FLGAGTACIADLTTFPDTAKVRLQIGESQGPVRATVSAQYGVMTITLWRTGEP 66
OY 69 SFWRGNLAVIRYPTALNFAFKDKYQIFLGVDKRTQFWRFYAGNLASGAAGATSL 128
DB 67 SLVNGLVAGLQRMSPASVRIGLYDSVKQFYTKSEHNS-----IGSLLAGSTTGALAV 121
OY 129 CFVYPLDEPARKLADYDGKAGAREFRGLDCLVKYIKSDGICKLYOGFNVSVGCIITIR 188
DB 122 AVAOPTVVKYRFQAO--ARAGGRRYOSTVNAVYRTIAREEGFRGLMGKTSFNVARNALVN 180
OY 189 AAYGIVDTAK-----GMLPDPKNTFHVISMIAQTAVAGLTSYFPTVRRMMQOS 242
DB 181 CAELVYTDLIKDALIKANLMTDLPCHFTSAFGAGFCTTYVAS----PVDVYKTRYNMSA 236
OY 243 -GRKGTIMYTGTLDCMKRIARDEGKAFFKGANSNVL-R-GMGAFVLYLYDEIKR 296
DB 237 LGQ-----YSSAGHCALTMLOKEGPRAFYKGFMPFSLRLGSMVNVMEVTEYQLKR 286

RESULT 14
US-08-470-868A-56
; Sequence 56, Application US/08470868A
; Patent No. 5861485
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis C.
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie and Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/470,868A
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7853-0031-999
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-8864
;; TELEX: 66441 PENNIE
;; INFORMATION FOR SEQ ID NO: 56:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 299 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;;
US-08-470-868A-56

Query Match 15.3%; Score 236.5; DB 2; Length 299;
Best local similarity 23.6%; Pred. No. 6.6e-19;
Matches 70; Conservative 57; Mismatches 142; Indels 27; Gaps 8;
;;
OY 12 FLAGVAAAIKSTAVAPIERVKLLQVOHASK---QITADQYGIIDCVIRIKDEVL 68
DB 7 FLGAGTACIADLTTFPDTAKVRLQIGESQGPVRATVSAQYGVMTITLWRTGEP 66
OY 69 SFWRGNLAVIRYPTALNFAFKDKYQIFLGVDKRTQFWRFYAGNLASGAAGATSL 128
DB 67 SLVNGLVAGLQRMSPASVRIGLYDSVKQFYTKSEHNS-----IGSLLAGSTTGALAV 121
OY 129 CFVYPLDEPARKLADYDGKAGAREFRGLDCLVKYIKSDGICKLYOGFNVSVGCIITIR 188
DB 122 AVAOPTVVKYRFQAO--ARAGGRRYOSTVNAVYRTIAREEGFRGLMGKTSFNVARNALVN 180
OY 189 AAYGIVDTAK-----GMLPDPKNTFHVISMIAQTAVAGLTSYFPTVRRMMQOS 242
DB 181 CAELVYTDLIKDALIKANLMTDLPCHFTSAFGAGFCTTYVAS----PVDVYKTRYNMSA 236
OY 243 -GRKGTIMYTGTLDCMKRIARDEGKAFFKGANSNVL-R-GMGAFVLYLYDEIKR 296
DB 237 LGQ-----YSSAGHCALTMLOKEGPRAFYKGFMPFSLRLGSMVNVMEVTEYQLKR 286

RESULT 15
US-08-775-009-32
; Sequence 32, Application US/08775009
; Patent No. 5935783
; GENERAL INFORMATION:
; APPLICANT: Gong, Wellong
; APPLICANT: Emanuel, Beverly S.
; APPLICANT: Budarf, Marcia L.
; APPLICANT: Roe, Bruce
; TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digeorge and
; TITLE OF INVENTION: Vellocardioloacial Syndrome Minimal Critical Region
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5935783rls, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775,009
FILING DATE: 27-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yalko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CH-0681
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-775-009-32
```

```
Query Match 15.0%; Score 232.5; DB 2; Length 311;
Best Local Similarity 27.8%; Pred. No. 2,1e-18;
Matches 84; Conservative 44; Mismatches 133; Indels 41; Gaps 11;

QY 10 KDFLAGVAAAIKSTAVAPIERVKLLQVHASKQITADKOYKGIIDCVRIIPKDOEVL 69
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 27 KALLAGLAGGIEICITFTPEYVKTLQDLERSH---PPRYRGIGDCVQTVRSHGVLG 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 70 FWRGLAVIRKFFQALNFA---FKDKYKQIFLGVDKRTQFMRYFAGNLASGAAGAT 126
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 LYRGLSLLYGSIKRAAVRFGMEFLSNHMRDQGRLDST-----RGLLGLGAGVAE 135

QY 127 SLCEFYPLDFARTRLAADVKGAGAEERFRLGDCLVKTIYKSDIKGLYOGFNVSY----- 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 AVVVVCPMETVVKRPIHD--QTSPPNPKYRGFFHGVREIYREGGLKGTQGLTATVLRKQGS 193
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 182 -QGIIYRAAYFGIYDTAKGMLPD-PKNTHTIVISWMAIQTVTAAGLTSY---PEDTVR 235
   | | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 194 NQAIRFF--VMTSLRNWYRGDNPNKPMNP-----LITGVFGALIGAASVFGNTPLDVIR 245

QY 236 RMMMQSGRKGDIMYTGTLDCWRKIARDEGKAFPKGAMSNVLR-GMGAGFVLYLYDEI 294
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 246 TRMOGLEAHK-----YRNTWDCGLQILKKEGLKAFYKGTFRPLRGVCLDVATVAVIYDEV 300
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 295 KK 296
   |
Db 301 YK 302
```

Search completed: November 12, 2002, 16:49:19
Job time : 13.0131 secs


```

OY 181 VGGIIIRAAVFGIYDTAKGMLDPKNTHTIVISWMIQOTYTAAGLTSYFEDTVRRMM 240
      |||||||
Db 181 VGGIIIRAAVFGIYDTAKGMLDPKNTHTIVISWMIQOTYTAAGLTSYFEDTVRRMM 240
OY 241 QSGRKGTDIMYTGTLDCWKRIARDEGGKAFKGMNSVLRGMGAFVLVLYDEIKKTT 298
      |||||||
Db 241 QSGRKGTDIMYTGTLDCWKRIARDEGGKAFKGMNSVLRGMGAFVLVLYDEIKKTT 298

```

RESULT 2

```

US-09-810-644-32
; Sequence 32, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Willey, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Scabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yazhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PR
; ORGANISM: Homo sapien
US-09-810-644-32

```

```

Query Match          100.0%; Score 1547; DB 10; Length 298;
Best Local Similarity 100.0%; Pred. No. 3,6e-154;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 MTDAAISFADFLAGGVAIAISKTAVAPIERVKLLLOVGHASKOITADKQYKGIIDCVR 60
      |||||||
Db 1 MTDAAISFADFLAGGVAIAISKTAVAPIERVKLLLOVGHASKOITADKQYKGIIDCVR 60
OY 61 IPKQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKRTQFMRYPAGNLASG 120
      |||||||
Db 61 IPKQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKRTQFMRYPAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLADVKGAGAREFRGLGDLVKIYKSDGIRKGLYQGFNS 180
      |||||||
Db 121 GAAGATSLCFVYPLDFARTRLADVKGAGAREFRGLGDLVKIYKSDGIRKGLYQGFNS 180
OY 181 VGGIIIRAAVFGIYDTAKGMLDPKNTHTIVISWMIQOTYTAAGLTSYFEDTVRRMM 240
      |||||||
Db 181 VGGIIIRAAVFGIYDTAKGMLDPKNTHTIVISWMIQOTYTAAGLTSYFEDTVRRMM 240
OY 241 QSGRKGTDIMYTGTLDCWKRIARDEGGKAFKGMNSVLRGMGAFVLVLYDEIKKTT 298
      |||||||
Db 241 QSGRKGTDIMYTGTLDCWKRIARDEGGKAFKGMNSVLRGMGAFVLVLYDEIKKTT 298

```

RESULT 3

```

US-09-811-094-33
; Sequence 33, Application US/09811094
; Patent No. US2001004414A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Willey, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Szabo, Tomas R.

```

```

; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yazhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PR
; ORGANISM: Homo sapien
US-09-811-094-33

```

```

Query Match          94.0%; Score 1454; DB 10; Length 298;
Best Local Similarity 92.6%; Pred. No. 1,9e-144;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

```

```

OY 1 MTDAAISFADFLAGGVAIAISKTAVAPIERVKLLLOVGHASKOITADKQYKGIIDCVR 60
      ||:|||||
Db 1 MTDAAISFADFLAGGVAIAISKTAVAPIERVKLLLOVGHASKOITADKQYKGIIDCVR 60
OY 61 IPKQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKRTQFMRYPAGNLASG 120
      |||||||
Db 61 IPKQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKRTQFMRYPAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLADVKGAGAREFRGLGDLVKIYKSDGIRKGLYQGFNS 180
      |||||||
Db 121 GAAGATSLCFVYPLDFARTRLADVKGAGAREFRGLGDLVKIYKSDGIRKGLYQGFNS 180
OY 181 VGGIIIRAAVFGIYDTAKGMLDPKNTHTIVISWMIQOTYTAAGLTSYFEDTVRRMM 240
      |||||||
Db 181 VGGIIIRAAVFGIYDTAKGMLDPKNTHTIVISWMIQOTYTAAGLTSYFEDTVRRMM 240
OY 241 QSGRKGTDIMYTGTLDCWKRIARDEGGKAFKGMNSVLRGMGAFVLVLYDEIKK 296
      |||||||
Db 241 QSGRKGTDIMYTGTLDCWKRIARDEGGKAFKGMNSVLRGMGAFVLVLYDEIKK 296

```

RESULT 4

```

US-09-810-644-33
; Sequence 33, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Willey, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Scabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yazhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PR
; ORGANISM: Homo sapien
US-09-810-644-33

```

```

Query Match          94.0%; Score 1454; DB 10; Length 298;
Best Local Similarity 92.6%; Pred. No. 1,9e-144;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

```

```

OY 1 MTDAAISFADFLAGGVAIAISKTAVAPIERVKLLLOVGHASKOITADKQYKGIIDCVR 60

```

RESULT 6

```

? Sequence 252, Application US/09801368
? Patent No. US20020128250A1
?
? GENERAL INFORMATION:
?
? APPLICANT: Busby, Robert
? APPLICANT: Cali, Brian
? APPLICANT: Hecht, Peter
? APPLICANT: Holtzman, Doug
? APPLICANT: Madden, Kevin
? APPLICANT: Maxon, Mary
? APPLICANT: Milne, Todd
? APPLICANT: No. US20020128250A1man, Thea
? APPLICANT: Royer, John
? APPLICANT: Salama, Sofie
? APPLICANT: Sherman, Amir
? APPLICANT: Silva, Jeff
? APPLICANT: Summers, Eric
? TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
? FILE REFERENCE: 109272.147
? CURRENT APPLICATION NUMBER: US/09/801.368
? CURRENT FILING DATE: 2001-03-07
?

```

;; PRIOR APPLICATION NUMBER: US 09/487,558
;; PRIOR FILING DATE: 2000-01-19
;; PRIOR APPLICATION NUMBER: US 60/160,587
;; PRIOR FILING DATE: 1999-10-20
;; NUMBER OF SEQ ID NOS: 440
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 252
;; LENGTH: 318
;; TYPE: PRT
;; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-252

Query Match 48.6%; Score 752.5; DB 10; Length 318;
Best Local Similarity 54.3%; Pred. No. 4,4e-71;
Matches 159; Conservative 40; Mismatches 85; Indels 9; Gaps 5;

Qy 7 SPADFLAGVAAASKRAVAPIERVKLLQVQ-HASKQIADKQYKIIICVRIPEQ 65
Db 22 NFLIDFLMGVSAAVAKTAASPIERVKLLIONODEMLKQGLDRLKRYAGILDCFKRTATOE 81
Qy 66 EVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRPAGNLASGAGA 125
Db 82 GVISFWRGNLANVIRYPTQALNFAFKDKIKAMF--GFKKEGVAKWFAGNLASGAGA 139
Qy 126 TSLCFVYPLDFARTRLAAD--VGKAGAREFRGIDCLVKIKYKSDGIKGLYOGFNVSQ 183
Db 140 LSLFVYSLDYARTRLAADSSKKGARQFNGLIDYKKTLSQVAGLYRGFLPSVYG 199
Qy 184 IIVRAAEGYIDTPAKG-MLPDPKNTHTVISMIAQTVTAAGLTSYFPDVRRRMMQ 242
Db 200 IIVRKGIFYGMDSLKPLLTGSLGSLASFLAGVVTGASTCSTYPLDVRRRMMTS 259
Qy 243 GRKGTIDIMYGTLDCKWRKIARDEGKAFKAGMSNVLRGMAFVLYDEIK 295
Db 260 GQA--VAYDGAFLDKRIVAEGVSLFKGCGANILKGVAGAGVISMVDQ 309

RESULT 8
US-09-734-569-170
;; Sequence 170, Application US/09734569
;; Patent No. US20020064816A1
;; GENERAL INFORMATION:
;; APPLICANT: Lerchl, Jens
;; APPLICANT: Renz, Andreas
;; APPLICANT: Ehrhardt, Thomas
;; APPLICANT: Reinhardt, Andreas
;; APPLICANT: Cirpus, Petra
;; APPLICANT: Bischoff, Friedrich
;; APPLICANT: Frank, Markus
;; APPLICANT: Freund, Annette
;; APPLICANT: Duvenig, Elke
;; APPLICANT: Schmidt, Ralf-Michael
;; APPLICANT: Reski, Ralf
;; TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
;; TITLE OR INVENTION: In the synthesis of carboxydrates
;; FILE REFERENCE: BASF-NAE-1332-99-US
;; CURRENT APPLICATION NUMBER: US/09/734,569
;; CURRENT FILING DATE: 2001-05-24
;; PRIOR APPLICATION NUMBER: US 60/177,101
;; PRIOR FILING DATE: 1999-12-16
;; NUMBER OF SEQ ID NOS: 181
;; SOFTWARE: PatentIn Ver. 2.1/WordPerfect 6.1
;; SEQ ID NO 170
;; LENGTH: 386
;; TYPE: PRT
;; ORGANISM: Physcomitrella patens
US-09-734-569-170

Query Match 47.9%; Score 741.5; DB 10; Length 386;
Best Local Similarity 53.4%; Pred. No. 8e-70;
Matches 157; Conservative 42; Mismatches 86; Indels 9; Gaps 5;

Qy 7 SFAKDLAGVAAAIKRAVAPIERVKLLQVQ-HASKQIADKQYKGIICVRIPEQ 65

Db 84 SFMTDFLMGVSAAVSKRAAPIERVKLLIONODEMLKSGRLSPHYKIGCFESRTYKDE 143
Qy 66 EVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRPAGNLASGAGA 125
Db 144 GMSLWRGNLANVIRYPTQALNFAFKDYKSLF--GTRKDDGYKWFAGNLASGAGA 202
Qy 126 TSLCFVYPLDFARTRLAADV--GKAGAREFRGIDCLVKIKYKSDGIKGLYOGFNVSQ 182
Db 203 LSLFVYSLDYARTRLAADSSKKGGERQFNGLVDYKKTLDGAGLYRGFLPSVYG 262
Qy 183 GIIVRAAEGYIDTPAKG-MLPDPKNTHTVISMIAQTVTAAGLTSYFPDVRRRMMQ 241
Db 263 GIIVRKGIFYGMDSLKPLLTGSLGSLASFLAGVVTGASTCSTYPLDVRRRMMT 322
Qy 242 SGRKGTIDIMYGTLDCKWRKIARDEGKAFKAGMSNVLRGMAFVLYDEIK 295
Db 323 SGEA--VKYGSMDAERKQILAKGASLFRGAGANILRAVAGAGVLSGTDQ 373

RESULT 9
US-09-925-301-1459
;; Sequence 1459, Application US/09925301
;; Patent No. US20020052308A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;; FILE REFERENCE: P106
;; CURRENT APPLICATION NUMBER: US/09/925,301
;; PRIOR FILING DATE: 2001-08-10
;; PRIOR APPLICATION NUMBER: PCT/US00/05882
;; PRIOR FILING DATE: 2000-03-08
;; PRIOR APPLICATION NUMBER: 60/124,270
;; PRIOR FILING DATE: 1999-03-12
;; NUMBER OF SEQ ID NOS: 1694
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1459
;; LENGTH: 132
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (115)
;; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (123)
;; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (126)
;; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (129)
;; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1459

Query Match 31.3%; Score 484; DB 10; Length 132;
Best Local Similarity 87.9%; Pred. No. 1.5e-43;
Matches 94; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MTDAAISFAKFLAGVAAAIKRAVAPIERVKLLQVQHSKQIADKQYKGIICVYR 60
Db 26 MTEQAISFAKFLAGVAAAIKRAVAPIERVKLLQVQHSKQIADKQYKGIICVIR 85
Qy 61 IPKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRT 107
Db 86 IPKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRT 132

RESULT 10
US-09-864-761-36440
;; Sequence 36440, Application US/09864761
;; Patent No. US20020048763A1
;; GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: A60124-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 36440
LENGTH: 87
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO L78810.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
OTHER INFORMATION: SWISSPROT HIT: P05141, EVALUE 6.00e-38
OTHER INFORMATION: EST_HUMAN HIT: AW935235.1, EVALUE 5.00e-37
US-09-864-761-36440

Query Match 29.0%: Score 448; DB 10: Length 87;
Best Local Similarity 100.0%: Pred. NO. 5.1e-40;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

113 FAGNLASGAGATSLCFVYPLDFARTRLAADVKGAGAREFRGLGDLVKIYKSDGIKG 172
|||||

Db 1 FAGNLASGAGATSLCFVYPLDFARTRLAADVKGAGAREFRGLGDLVKIYKSDGIKG 60
Qy 173 LYGFNNSVOCIIITYRAAYFGIYDTAK 199
Db 61 LYGFNNSVOCIIITYRAAYFGIYDTAK 87

RESULT 11
US-09-777-921A-2
Sequence 2, Application US/09777921A
Patent No. US20020115136A1
GENERAL INFORMATION:
APPLICANT: MERKULOV et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
FILE REFERENCE: CL001103
CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 477
TYPE: PRT
ORGANISM: Homo sapiens
US-09-777-921A-2

Query Match 22.7%: Score 351; DB 10: Length 477;
Best Local Similarity 31.5%: Pred. No. 7e-29;
Matches 93; Conservative 61; Mismatches 113; Indels 28; Gaps 10;

Qy 10 KDFLAGCAAAISTAAPIRVRVLLQOVHASKQITRDKRYKIIIDCVNIPREOEVL 69
Db 196 RQLLAGGIAGAVSRTSAPLRLKIMQV-HGSK--SDKM--NIFGFRQVREGGIRS 249
Qy 70 FMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFVRYPAGNLASGAGATSLC 129
Db 250 LMRNGNVTIATPETAIVKFAVQYKLLREBQOKICTFFRFTSGSR----AGATROT 304
Qy 130 FVYPLDFARTRLAADVKGAGAREFRGLGDLVKIYKSDGIKGLYGFNNSVOCIIITYRA 189
Db 305 FIYPMEVWKTRLA--VGKTG--OYSGIYDCAKKILKHEGIGAFYKGVPMILGIIPYAG 359
Qy 190 AVEFIYDTAK-----GMLPDPKNIHIVSMIAQTVNAVAGLTSPPTVYRRMMOSGR 244
Db 360 IDLAVELKLSYWLNDRAKDSVNGVAVLLCGALLSTCGQLASPLALVTRMQAQA 419
Qy 245 KGTDIMYGTLDCKWRIARDEGKAFKFGANSN---VLRGAGAFVLVYDEIKK 296
Db 420 EGSFQL--NMVGLFRRIISKIGIYGLVGRITPNFMKVLPAVGISY--VYENMQ 470

RESULT 12
US-09-777-921A-4
Sequence 4, Application US/09777921A
Patent No. US20020115136A1
GENERAL INFORMATION:
APPLICANT: MERKULOV et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
FILE REFERENCE: CL001103
CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 475
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-09-777-921A-4

Query Match 22.6%: Score 350; DB 10: Length 475;

Best Local Similarity 31.2%; Pred. No. 8.9e-29;
Matches 92; Conservative 59; Mismatches 114; Indels 30; Gaps 9;
QY 10 KDLAGVAAAIKSTAVAPIEVKKLLQVHASKQITADKQYKGIIDCVVRIPKQEVLS 69
Db 196 ROLLAGGAGAVASRTSTAPLDRLKIMQV-HGSKM--NIFGFRQWKEGIRS 247
QY 70 FWRGNLAVIRFPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASGAAGATSLC 129
Db 248 LMRGNGTVIIRAPETAVKFMVYEQYKLLTEEGKIGTFEFTISGM-----AGATQOT 302
QY 130 FVYPLDFARTLADYKAGAEERFGLDCLVKIYKSDGKIKLYGQFNVSVOGIITIRA 189
Db 303 FLYPEVAKTRILA--VGKRG--QYSGIYDCAKKIKLYEGFGAFKGYVPMNLGITIPYAG 357
QY 190 AVFGIYDRAK-----GMLPDKNTHIVISMTAQVTAVAGLTSVPDTPVRRMMQSGR 244
Db 358 IDLAVYELLSHMDNPAKDSVNPGLVLLGCGALSTCGQLASTPLALVTRMQAQL 417
QY 245 KGTDMYGTGLDCWKRKIRADEGKAFKAGMSN--VLRMGCAFVLVLYDEIKR 296
Db 418 ECAQPL--NMVGLFRRIITSKEQLPGLYRGITPNEFKVLPVAGISV--VYENMKQ 468

RESULT 13
US-09-777-921A-5
; Sequence 5, Application US/09777921A
; Patent No. US20020115136A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: CLO001103
; CURRENT APPLICATION NUMBER: US/09/777,921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-777-921A-5
Query Match 20.9%; Score 323.5; DB 10; Length 410;
Best Local Similarity 33.6%; Pred. No. 4.3e-26;
Matches 80; Conservative 46; Mismatches 91; Indels 21; Gaps 7;
QY 10 KDLAGVAAAIKSTAVAPIEVKKLLQVHASKQITADKQYKGIIDCVVRIPKQEVLS 69
Db 189 ROLLAGGAGAVASRTSTAPLDRLKIMQV-HGSKM--NIFGFRQWKEGIRS 242
QY 70 FWRGNLAVIRFPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASGAAGATSLC 129
Db 243 LMRGNGTVIIRAPETAVKFMVYEQYKLLTEEGKIGTFEFTISGM-----AGATQOT 297
QY 130 FVYPLDFARTLADYKAGAEERFGLDCLVKIYKSDGKIKLYGQFNVSVOGIITIRA 189
Db 298 FLYPEVAKTRILA--VGKRG--QYSGIYDCAKKIKLYEGFGAFKGYVPMNLGITIPYAG 352
QY 190 AVFGIYDRAK-----GMLPDKNTHIVISMTAQVTAVAGLTSVPDTPVRRMMQSGR 242
Db 353 IDLAVYELLSHMDNPAKDSVNPGLVLLGCGALSTCGQLASTPLALVTRMQAQL 410
RESULT 14
US-09-992-598-289
; Sequence 289, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C20
CURRENT APPLICATION NUMBER: US/09/992,598
PRIOR APPLICATION NUMBER: 2001-11-14
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202

[illegible]

RESULT 15
US-09-989-722-289
Sequence 289, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Raoul, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349

```
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090576
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
```

Query Match 19.5%; Score 302; DB 10; Length 469;
Best Local Similarity 29.1%; Pred. No. 9.1e-24;
Matches 86; Conservative 60; Mismatches 118; Indels 32; Gaps 11;

```
OY 10 KDFLAGVAAIASTAVAPIERVLLQVOHASKOITADKOYGIIDCVRIPEQEVLS 69
Db 188 RHVLVAGGAGAVSRCTCAPDRLKVLMOV-HASR----SNNMGIVGGFTOMIREGARS 241
OY 70 FMRGNLANVIRYPTQALNFAFKDKYKOIFLGVDKRTQFWRYPAGNLAGSAGAGATSLC 129
Db 242 LMRNGINVLKIAPESAIKFPAFYQIKR--LVGSDQET---LRIHERLVAGSLAGATAQS 296
OY 130 FVYPLDFARTRLADVKGAGAEFRGLGDCLVKIRKSDGIKGLYOGFNNVSGIITYRA 189
Db 297 SIYPMEVILKTRMA--LKRKTG---QYSGMLDCARILAREGVAAFYKGVVPMGLIIPYAG 351
```

```
OY 190 AVEGIYDTAKM-----LPDPKNTHIVISMIAQTVTAVAG-LTSYPEDTVRRRAM 240
Db 352 IDLAVYETLKNAMLOHYAVNSADPG---VFVLLACGTMSSTCGQLASYPALVTRMOA 407
OY 241 QSGRKGTDIMYTGFLDCWRKIADEGGKAFKGAWSNVLRGMGAFV-LVLYDEIK 295
Db 408 QASIEGAPEVTMSSL--FKHILRTGAFGLYRGLAPNFMKVIYPAVSISYVYENLK 461
```

Search completed: November 12, 2002, 16:56:56
Job time : 7.34043 secs

Db 181 VGGIITIRAAAFGIYDPAKGMILPDPKNTHTVISMIAQVTAVAGLTSYPEDTVRRMM 240
 QY 241 QSGRKGTDIMVTGTLDCWRKILARDEGKAFKGMAMSVNLRMGAFVLYLVDELTKKYT 298
 Db 241 QSGRKGTDIMVTGTLDCWRKILARDEGKAFKGMAMSVNLRMGAFVLYLVDELTKKYT 298

RESULT 2

S31814

ADP, ATP carrier protein T2 - mouse

N:Alternate names: adenine nucleotide translocase

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998

C:Accession: S31814

R:Costet, P.; Laplace, C.

A:Reference number: S31814

A:Accession: S31814

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-298 <COS>

A:Cross-references: EMBL:X70847

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACPI>

F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP>

F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match

Best Local Similarity 95.6%; Score 1479; DB 2; Length 298;

Matches 285; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAIASTKTAAPIERVKLLQVHASKOITADKOYKGIIDCVR 60
 Db 1 MTDAAVSPAKDFLAGVAAIASTKTAAPIERVKLLQVHASKOITADKOYKGIIDCVR 60
 QY 61 IPKQEVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
 Db 61 IPKQGVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
 QY 121 GAAGATSCFEPYPLDFARTRLAADVGRKAGAEFERGLGDCLVKTKSGIKGLYQGFNV 180
 Db 121 GAAGATSCFEPYPLDFARTRLAADVGRKAGAEFERGLGDCLVKTKSGIKGLYQGFNV 180
 QY 181 VGGIITIRAAAFGIYDPAKGMILPDPKNTHTVISMIAQVTAVAGLTSYPEDTVRRMM 240
 Db 181 VGGIITIRAAAFGIYDPAKGMILPDPKNTHTVISMIAQVTAVAGLTSYPEDTVRRMM 240
 QY 241 QSGRKGTDIMVTGTLDCWRKILARDEGKAFKGMAMSVNLRMGAFVLYLVDELTKKYT 298
 Db 241 QSGRKGTDIMVTGTLDCWRKILARDEGKAFKGMAMSVNLRMGAFVLYLVDELTKKYT 298

RESULT 3

ADP, ATP carrier protein T2 - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999

C:Accession: B43646

R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.

Biochemistry 28, 866-873, 1989

A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in

A:Reference number: A43646; MUID:8922093; PMID:2540808

A:Accession: B43646

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-298 <POW>

A:Cross-references: GB:M42403; NID:9529416; PIDN:AAA30769.1; PID:9529417

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein

F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACPI>

F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP>

F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match

Best Local Similarity 94.2%; Score 1458; DB 2; Length 298;

Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAIASTKTAAPIERVKLLQVHASKOITADKOYKGIIDCVR 60
 Db 1 MTEQAISPAKDFLAGIAAIASTKTAAPIERVKLLQVHASKOITADKOYKGIIDCVR 60
 QY 61 IPKQEVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
 Db 61 IPKQGVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
 QY 121 GAAGATSCFEPYPLDFARTRLAADVGRKAGAEFERGLGDCLVKTKSGIKGLYQGFNV 180
 Db 121 GAAGATSCFEPYPLDFARTRLAADVGRKAGAEFERGLGDCLVKTKSGIKGLYQGFNV 180
 QY 181 VGGIITIRAAAFGIYDPAKGMILPDPKNTHTVISMIAQVTAVAGLTSYPEDTVRRMM 240
 Db 181 VGGIITIRAAAFGIYDPAKGMILPDPKNTHTVISMIAQVTAVAGLTSYPEDTVRRMM 240
 QY 241 QSGRKGTDIMVTGTLDCWRKILARDEGKAFKGMAMSVNLRMGAFVLYLVDELTK 296
 Db 241 QSGRKGTDIMVTGTLDCWRKILARDEGKAFKGMAMSVNLRMGAFVLYLVDELTK 296

RESULT 4

ADP, ATP carrier protein T3 - human

N:Alternate names: ADP, ATP carrier protein T2 (misidentification); mitochondrial ADP,

C:Species: Homo sapiens (hmn)

C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000

C:Accession: S03894; B28116

R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.

J. Mol. Biol. 206, 261-280, 1989

A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP

A:Reference number: S03893; MUID:89236396; PMID:2541251

A:Accession: S03894

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-298 <COZ>

R:Houldsworth, J.; Altardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1

A:Reference number: A94197; MUID:88124845; PMID:2829183

A:Accession: B28116

A:Molecule type: mRNA

A:Residues: 36-104, 'R', '106', 'A', '109-298 <HOZ>

A:Cross-references: GB:J03592; NID:g339722; PIDN:AAA36750.1; PID:g339723

A:Experimental source: liver

C:Genetics:

A:Gene: GDB:ANT3; ANT3Y

A:Cross-references: GDB:125184; OMIM:300151; OMIM:403000

A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3

A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein

F:2-298/Product: ADP, ATP carrier protein #status predicted <MAT>

F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACPI>

F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match

Best Local Similarity 94.0%; Score 1454; DB 1; Length 298;

Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAIASTKTAAPIERVKLLQVHASKOITADKOYKGIIDCVR 60
 Db 1 MTEQAISPAKDFLAGIAAIASTKTAAPIERVKLLQVHASKOITADKOYKGIIDCVR 60
 QY 61 IPKQEVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
 Db 61 IPKQGVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120

Db 61 IPKRGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRNQFWRYFAGNLSG 120
 QY 121 GAAGATSLCFYPPIDFARTRLAADVGKAGAEERERGLGDCLVKTKYSDGKGLYOGFNVS 180
 Db 121 GAAGATSLCFYPPIDFARTRLAADVGKAGAEERERGLGDCLVKTKYSDGKGLYOGFNVS 180
 QY 181 VGGIITIRAAAFVGYDPAKGMPLPDKNTHIVSMIAQTVAVAGLVSYPEDTVRRRMM 240
 Db 181 VGGIITIRAAAFVGYDPAKGMPLPDKNTHIVSMIAQTVAVAGLVSYPEDTVRRRMM 240
 QY 241 QSGRKGADIMYTGTLDCWRKIADEGKAFKFGKAMSNNLRMGCAFVLVLYDEIKK 296
 Db 241 QSGRKGADIMYTGTLDCWRKIADEGKAFKFGKAMSNNLRMGCAFVLVLYDEIKK 296

RESULT 5

ADP/ATP carrier protein T1 - bovine
 N:Alternate names: ADP/ATP translocase T1
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999
 C:Accession: A43646; A24822; A03181; A61343; S69369
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093; PMID:2540808
 A:Accession: A43646
 A:Molecule type: mRNA
 A:Residues: 1-298 <PDM>
 A:Cross-references: GB:M24102; NID:g529414; PID:AAA30768.1; PID:g529415
 R:Rasmussen, U.B.; Mohlrah, H.
 Biochem. Biophys. Res. Commun. 138, 850-857, 1986
 A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual
 A:Reference number: A24822; MUID:8629375; PMID:3017341
 A:Accession: A24822
 A:Molecule type: mRNA
 A:Residues: 208-298 <RAS>
 A:Cross-references: GB:M13783; NID:g162630; PID:AAA30363.1; PID:g162631
 R:Aquila, H.; Mistr, D.; Eulitz, M.; Klingenberg, M.
 Hoppe-Seyler's Z. Physiol. Chem. 363, 343-349, 1982
 A:Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria
 A:Reference number: A03181; MUID:82188267; PMID:7076130
 A:Accession: A03181
 A:Molecule type: Protein
 A:Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298 <ANQ>
 A:Note: residue 52 may be methyllysine
 R:Bebel, W.; Wächter, E.; Aquila, H.; Klingenberg, M.
 Biochim. Biophys. Acta 670, 176-180, 1981
 A:Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondria
 A:Reference number: A61343; MUID:82046808; PMID:6271240
 A:Accession: A61343
 A:Molecule type: Protein
 A:Residues: 205-298 <BAB>
 R:Oetmeier, W.; Masson, K.; Kallina, S.
 Eur. J. Biochem. 227, 730-733, 1995
 A:Title: [(3)H]-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP
 A:Reference number: S69369; MUID:55172050; PMID:7867632
 A:Accession: S69369
 A:Molecule type: Protein
 A:Residues: 49-63,154-168 <OET>
 C:Comment: This protein is synthesized in the cytosol and transported into the mitochondrion
 C:Complex: homodimer
 C:Function:
 A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
 A:Note: Located in the inner mitochondrial membrane
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitoch
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 91.7%; Score 1419; DB 1; Length 298;
 Best Local Similarity 89.9%; Pred. No. 9.5e-119;
 Matches 267; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTDALSFPAKDLGVAALSKTAVAPIERVKLLQVHASKOITADKQKGIIDCVR 60
 Db 1 MSDALSFPAKDLGVAALSKTAVAPIERVKLLQVHASKOITADKQKGIIDCVR 60
 QY 61 IPKDEVLSEFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRNQFWRYFAGNLSG 120
 Db 61 IPKDEVLSEFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRNQFWRYFAGNLSG 120
 QY 121 GAAGATSLCFYPPIDFARTRLAADVGKAGAEERERGLGDCLVKTKYSDGKGLYOGFNVS 180
 Db 121 GAAGATSLCFYPPIDFARTRLAADVGKAGAEERERGLGDCLVKTKYSDGKGLYOGFNVS 180
 QY 181 VGGIITIRAAAFVGYDPAKGMPLPDKNTHIVSMIAQTVAVAGLVSYPEDTVRRRMM 240
 Db 181 VGGIITIRAAAFVGYDPAKGMPLPDKNTHIVSMIAQTVAVAGLVSYPEDTVRRRMM 240
 QY 241 QSGRKGADIMYTGTLDCWRKIADEGKAFKFGKAMSNNLRMGCAFVLVLYDEIKK 297
 Db 241 QSGRKGADIMYTGTLDCWRKIADEGKAFKFGKAMSNNLRMGCAFVLVLYDEIKK 297

RESULT 6

ADP/ATP carrier protein T1 - mouse
 N:Alternate names: adenine nucleotide carrier
 C:Species: Mus musculus (house mouse)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
 C:Accession: S37210
 R:Laplace, C.; Costet, P.
 submitted to the EMBL Data Library, September 1993
 A:Reference number: S37210
 A:Accession: S37210
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <LNP>
 A:Cross-references: EMBL:X74510; NID:g402627; PID:CAA52616.1; PID:g402628
 C:Genetics:
 A:Gene: ANCL
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 91.6%; Score 1417; DB 2; Length 298;
 Best Local Similarity 89.6%; Pred. No. 1.4e-118;
 Matches 266; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTDALSFPAKDLGVAALSKTAVAPIERVKLLQVHASKOITADKQKGIIDCVR 60
 Db 1 MGDALSFPAKDLGVAALSKTAVAPIERVKLLQVHASKOITADKQKGIIDCVR 60
 QY 61 IPKDEVLSEFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRNQFWRYFAGNLSG 120
 Db 61 IPKDEVLSEFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRNQFWRYFAGNLSG 120
 QY 121 GAAGATSLCFYPPIDFARTRLAADVGKAGAEERERGLGDCLVKTKYSDGKGLYOGFNVS 180
 Db 121 GAAGATSLCFYPPIDFARTRLAADVGKAGAEERERGLGDCLVKTKYSDGKGLYOGFNVS 180
 QY 181 VGGIITIRAAAFVGYDPAKGMPLPDKNTHIVSMIAQTVAVAGLVSYPEDTVRRRMM 240
 Db 181 VGGIITIRAAAFVGYDPAKGMPLPDKNTHIVSMIAQTVAVAGLVSYPEDTVRRRMM 240
 QY 241 QSGRKGADIMYTGTLDCWRKIADEGKAFKFGKAMSNNLRMGCAFVLVLYDEIKK 297
 Db 241 QSGRKGADIMYTGTLDCWRKIADEGKAFKFGKAMSNNLRMGCAFVLVLYDEIKK 297

```

RESULT 7
160173
adenine nucleotide translocator - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C:Accession: 160173
R:Shinozuka, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
Biochim. Biophys. Acta 1152, 192-196, 1993
A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat
A:Reference number: 160173; MUID:94002161; PMID:8399300
A:Accession: 160173
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-298 <RES>
A:Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA43842.1; PID:g400427
C:Genetics:
A:Gene: antl
A:Introns: 37/3; 200/1; 247/1
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match          91.6%; Score 1417; DB 2; Length 298;
Best Local Similarity 89.6%; Pred. No. 1.4e-118;
Matches 266; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTDALSPKDFLAGVAAAIKSTNAPLERKLLQVHASKQITADKQYGIIDCYVR 60
DB 1 MGDQALSPKDFLAGVIAAVSKTAVAPLERKLLQVHASKQISAEKQYGIIDCYVR 60
QY 61 IRKEQEVLSFWMGNLANVRYPTQALNFAFKDKYKQIFLGVDKRTQPMRFAGNLASG 120
DB 61 IRKEQGFSLFWMGNLANVRYPTQALNFAFKDKYKQIFLGVDKRTQPMRFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLADYKAGAEERFGLGDCLVKIKYKSDIKGLYOGFNV 180
DB 121 GAAGATSLCFVYPLDFARTRLADYKAGAEERFGLGDCLVKIKYKSDIKGLYOGFNV 180
QY 181 VOGIITIRAAFGYIDTAAGMLPDPKNTHTIVSMIAQVTVAGITVPTPTVRRMM 240
DB 181 VOGIITIRAAFGYIDTAAGMLPDPKNTHTIVSMIAQVTVAGITVPTPTVRRMM 240
QY 241 QSGRKGTIDIMYGTLDCKWRKIARDEGKAFKFGANSNVLKMGCAFVLVLYDEIKKY 297
DB 241 QSGRKGTIDIMYGTLDCKWRKIARDEGKAFKFGANSNVLKMGCAFVLVLYDEIKKY 297

RESULT 8
A44778
ADP,ATP carrier protein T1 - human
N:Alternate names: mitochondrial ADP,ATP translocase 1
C:Species: Homo sapiens (man)
C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: A44778; S03893; A39891; A28116
R:Li, K.; Warner, C.K.; Hodges, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.
J. Biol. Chem. 264, 13998-14004, 1989
A:Title: A human muscle adenine nucleotide translocator gene has four exons, is located
A:Reference number: A44778; MUID:89340499; PMID:2541778
A:Accession: A44778
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-298 <LIA>
A:Cross-references: GB:J04982; NID:9178658; PIDN:AAA51736.1; PID:9178659
R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr
A:Reference number: S03893; MUID:89236396; PMID:2541251
A:Accession: S03893
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <COZ>

```

```

R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A:Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a lea
A:Reference number: A39891; MUID:88041149; PMID:2823266
A:Accession: A39891
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>
A:Cross-references: GB:J02966; NID:9339919; PIDN:AAA61223.1; PID:9339920
A:Experimental source: clone PHMAN1
R:Houldsworth, J.; Attardi, G. 85, 377-381, 1988
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level i
A:Reference number: A94197; MUID:86124845; PMID:2829183
A:Accession: A28116
A:Molecule type: mRNA
A:Residues: 1-37 <HOU>
A:Cross-references: GB:J03593; NID:9339724; PIDN:AAA36751.1; PID:9339725
A:Experimental source: liver
C:Genetics:
A:Gene: GDB:ANT1; T1
A:Cross-references: GDB:119680; OMIM:103220
A:Map position: 4q35-4q35
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:2-398/Product: ADP,ATP carrier protein status predicted <MAT>
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match          91.3%; Score 1413; DB 1; Length 298;
Best Local Similarity 89.2%; Pred. No. 3.3e-118;
Matches 265; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTDALSPKDFLAGVAAAIKSTNAPLERKLLQVHASKQITADKQYGIIDCYVR 60
DB 1 MGDHMSFLKDFLAGVAAAVSKTAVAPLERKLLQVHASKQISAEKQYGIIDCYVR 60
QY 61 IRKEQEVLSFWMGNLANVRYPTQALNFAFKDKYKQIFLGVDKRTQPMRFAGNLASG 120
DB 61 IRKEQGFSLFWMGNLANVRYPTQALNFAFKDKYKQIFLGVDKRTQPMRFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLADYKAGAEERFGLGDCLVKIKYKSDIKGLYOGFNV 180
DB 121 GAAGATSLCFVYPLDFARTRLADYKAGAEERFGLGDCLVKIKYKSDIKGLYOGFNV 180
QY 181 VOGIITIRAAFGYIDTAAGMLPDPKNTHTIVSMIAQVTVAGITVPTPTVRRMM 240
DB 181 VOGIITIRAAFGYIDTAAGMLPDPKNTHTIVSMIAQVTVAGITVPTPTVRRMM 240
QY 241 QSGRKGTIDIMYGTLDCKWRKIARDEGKAFKFGANSNVLKMGCAFVLVLYDEIKKY 297
DB 241 QSGRKGTIDIMYGTLDCKWRKIARDEGKAFKFGANSNVLKMGCAFVLVLYDEIKKY 297

RESULT 9
S31935
ADP,ATP carrier protein - African malaria mosquito
C:Species: Anopheles gambiae (African malaria mosquito)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S31935; S31936
R:Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H.
submitted to the EMBL Data Library, February 1993
A:Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae
A:Reference number: S31935
A:Accession: S31935
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-301 <BEA>
A:Cross-references: EMBL:Z21814; EMBL:Z21815
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
F:7-101/Domain: ADP,ATP carrier protein repeat homology <ACP1>

```


F;112-204/Domain:	ADP,ATP carrier protein repeat	<ACP2>
F;209-300/Domain:	ADP,ATP carrier protein repeat	<ACP3>

Query Match	75.6%;	Score 1170;	DB 1;	Length 301;
Best Local Similarity	78.1%;	Pred. No. 1.4e-96;		
Matches 225;	Conservative 18;	Mismatches 45;	Indels 0;	Gaps 0;

Qy	8	FAFELFGLGVAAMIAISKRAVAPIEBEVKLLLOVHQAASKITADKQKGIIDCVBILPEQEV	67
Db	10	FAKDFELGGISAAASKRAVAPIEIVKLLLOVQAASKIAVDKQKGGVDCVFRPREQGI	69
Qy	68	LSEFGRMLIANVIRYFPTQALNFAFKDKYKQIFLGGVDKRYQFWRYPAGNLAASGAAGATS	127
Db	70	GAFCGMLIANVIRYFPTQALNFAFKDYKQYVFLGGVDKNTQFWRYFLGNLSGGAAGATS	129
Qy	128	LCFYFPLDFPARTRLAALVGVKAGAREERKGLDCLVYIKKSDGIKGLYQGRNVSVQGITIY	187
Db	130	LCFYFPLDFPARTRLGAOVGVGACGEREPENGLDCLCKTKVKKSDGIIIGLRGNVSVQGITIY	189
Qy	188	RAAFYGYTDAKGMILPDKMNTHTIYSMIAIQTVAYVAGLTSPEPDYRRRRMMQSGRGT	247
Db	190	RAAFYGFGEPTDAKGMILPDKMNTSIVSVMAIQVYTTAGIISTYEPDIYRRRRMMQSWCKS	249
Qy	248	DIWYTGILDCMRKTADEGGKAFKFGAMSVNLKMGCAFVLVLYDELK	295
Db	250	EWYTKNMLDCMWKIGKQEGSGAFKFGFNSVNLRTGALVLVYDEVK	297

RESULT 10
T25371

hypothetical protein T27E9.1 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T25371
R:Lloyd, C.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20024
A:Accession: T25371
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-300 <WTL>
A:Cross-references: EMBL:Z82059; PIDD:CA804874.1; GSPDB:GN00021; CESP:T27E9.1
A:Experimental source: clone T27E9
C:Genetics:
A:Gene: CESP:T27E9.1
A:Map position: 3
A:Introns: 20/1; 41/3; 115/2
A:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homoloid

	Query Match	66.7%;	Score 1032;	DB 2;	Length 300;
	Best Local Similarity	69.8%;	Pred.	N.1m.2.8e-84;	
	Matches 203;	Conservative 34;	Mismatches 50;	Indels 4;	Gaps 3;
OY	8 FAKDELACGVAASKTAVAPIERKLLQVONHASKOITADMOYKGIIIDCVIRIKREDEV	67			
Db	12 FLIDIASGGTAAASKVAPIERKLLQVODASKAIVADRKYGMIVLLRVREQDEV	71			
OY	68 LSPFRGNLANYIRFPTALNFAFDKDYKOJIFLGSDVKRTPORRFYFAGCLASGAAGATS	127			
Db	72 AALMRGNLANIYRIFFPTAMNFAPEDTYKAIFLEGLDKDDPKWKFPAQLLASGAAGATS	131			
OY	128 LCFVYPPLDFARTRLADYGAKAGEREFGDLCKLYIKYSDSIGKLGYOFNVNSVOGIILY	187			
Db	132 LCFVYPLDFAFTRLADIGKAN-DREFRGDLCDCLKLYKSOSPIGLNRGFYSVOGIILY	190			
OY	188 RAATFGIYDTAKML-PDPKNTHIYISMAIOATTVAVAGLSYPRPDYVRRMMMSGKKG	246			
Db	191 RAAFYGMDFTKMVFASDGOKINFEFAANGIAQVYTVGSIGLSYPMDTVFRMMMSGKR-	249			
OY	247 TDIMWTGLDLMCRKIARDECGAFPKGAMSUNLRBMGCATVLVLTDELKXY	297			
Db	250 -DILYKNTLDCAKTLIQNEGMSAMKGLSLNFRGTGGLAIYAIDELOKE	299			

RESULT 11

hypothetical protein K01H12.2 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: J23207
R:McMurray, A.
submitted to the EMBL Data Library, December 1995
A:Reference number: J19707
A:Accession: J23207
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-513 <WIL>
A:Cross-references: EMBL:Z66218; PDB:CAA92A72.1; GSPDB:GNO00022; CESP:K01H12.2
A:Experimental source: clone K01H12
C:Genetics:
A:Gene: CESP:K01H12.2
A:Map position: 4
A:Introns: 4/1, 191/2
A:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology

Qy	8	FANDELAGGVAANAISKTA	VAARIEBVKLLLOV	HAHKSQITADKOYKGIIDCV	VRPRKEQEV	67
Db	25	FLIDLASAGTAAASKT	VAARIEBVKLLLOV	HAHKSQITADKOYKGIIDCV	VRPRKEQEV	84
Qy	68	LSFMGNLANIYRFP	PTQALNFAEKDKYQJ	IFELGVDKRTQFMR	FAGNULASGGAATS	127
Db	85	AALMRGNLANIYRFP	PTQALNFAEKDYKNI	FQGLDKKQOFMK	FAGNULASGGAATS	144
Qy	128	LCFYVPLDEAFTR	LAADVGRKAGARE	RRGLDCLVYKIK	YSKIGLYOGFVNSVQGIIT	187
Db	145	LCFYVPLDEAFTR	LAADVGRKAGARE	RRGLDCLVYKIK	YSKIGLYOGFVNSVQGIIT	203
Qy	188	RAAYGIDTDAKGM	L-PDPKNTHTIYIS	SMIAIOQTVAAG	LSYSPEDYVRRRMMQOSRGK	246
Db	204	RAAYGIDTDAKGM	L-PDPKNTHTIYIS	SMIAIOQTVAAG	LSYSPEDYVRRRMMQOSRGK	265
Qy	247	TDIMYTGILDCW	KRIARDEGSKAF	FFKGMASVNLG	MGAFVLYLYDEIKY	297
Db	263	DVEKNTLDCAVK	IKNEGMSAMFKG	LSVYFGTGGAL	VALATYDEIOFR	312

RESULT 12
T25850

hypothetical protein T01B11.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: J25850
R:Geisels, C.; Stellyes, L.
submitted to the EMBL Data Library, December 1996
A:Description: The sequence of *C. elegans* cosmid T01B11.
A:Reference number: J20099
A:Accession: J25850
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-313 <GET>
A:Cross-references: EMBL:U80931, PIDN:AA838001.1, GSPDB:GN00022; CESP:T01B11.4
A:Experimental source: strain Bristol N2; clone T01B1
C:Genetics:
A:Gene: CESP:T01B11.4
A:Map position: 4
A:Introns: 4/1: 19/2
C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology

Query Match 66.5%; Score 1029; DB 2; Length 313;
Best Local Similarity 70.8%; Pred. NO. 5.5e-84;
Matches 206; Conservative 28; Mismatches 53; Indels 4; Gaps 3;

Db 63 RVSKDQGVLSLRGNVANVIRFPTQAFNFAKDYFNIF-PRYDQNTD3SKFCVNILS 121
Qy 120 GGAGATSLCFVYPLDFARTPLADVGKAGAREFRGLGDLVKYKSD3IKGLYQGFNV 179
Db 122 GATGATSLILYVPLDFARTPLASDICK-GKDRQFTGLFDCIAKIKOT3GLSLYSGFV 180
Qy 180 SVOGIIYRAAYFGIYDFAKGM-L-PDPKNTIHIVSMIAQTVTAAGLTSYPEDTVRRRM 238
Db 181 SVTGIIYRGSIYFGLYDSAKALLFTNDKNTNIVLKMVAQSVTILAGLISYEPEDTVRRRM 240
Qy 239 MMOSGRKG-TDIMYTGTLDCWRKILARDEGKAFFKANSNVLKMGGAFLVLYDEIKK 296
Db 241 MMSGRKKEEIOYKNTIDCWIKILRNKGFKEGKAMANVIRGAGALVLYVDELOK 299

Search completed: November 12, 2002, 16:48:37
Job time : 15.0157 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:43:20 ; Search time 7.67525 Seconds
(without alignments)
1610.364 Million cell updates/sec

Title: US-09-393-441-32
Perfect score: 1547
Sequence: 1 MTDALSFADFLAGVAA.....LRMGAFVLVYDEIKKYT 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1537	99.4	298	1	ADPT2_HUMAN
2	1525	98.6	298	1	ADPT2_RAT
3	1519	98.2	298	1	ADPT2_MOUSE
4	1458	94.2	298	1	ADPT3_BOVIN
5	1454	94.0	298	1	ADPT3_HUMAN
6	1417	91.6	298	1	ADPT1_MOUSE
7	1417	91.6	298	1	ADPT1_RAT
8	1414	91.4	297	1	ADPT1_BOVIN
9	1413	91.3	298	1	ADPT1_HUMAN
10	1218.5	76.9	297	1	ADPT_DROME
11	1190	76.8	301	1	ADPT_ANOGA
12	968	62.6	339	1	ADPT_CHLKE
13	771	49.8	386	1	ADPT1_GOSHI
14	770	49.8	322	1	ADPT_SCHPO
15	765	49.5	308	1	ADPT_CHLRE
16	761.5	49.2	307	1	ADPT3_YEAST
17	759	49.1	387	1	ADPT1_MAIZE
18	757	48.9	313	1	ADPT_NEUCR
19	753.5	48.7	385	1	ADPT2_ARATH
20	753	48.7	387	1	ADPT2_MAIZE
21	752.5	48.6	318	1	ADPT2_YEAST
22	752	48.6	386	1	ADPT1_SOLFU
23	750	48.5	382	1	ADPT1_SOLFU
24	749.5	48.4	305	1	ADPT_ORYSA
25	747.5	48.3	381	1	ADPT1_KUOLA
26	744	48.1	331	1	ADPT1_ARATH
27	741.5	47.9	386	1	ADPT2_SOLFU
28	737	47.6	331	1	ADPT2_WHEAT
29	728	47.1	309	1	ADPT1_YEAST
30	307	19.8	588	1	CMC2_CAEEL
31	302	19.5	587	1	CMC3_CAEEL
32	285	18.4	330	1	GDC_BOVIN
33	284	18.4	307	1	ODC2_YEAST

34	278	18.0	325	1	UCP5_MOUSE	092b2 mus musculu
35	276.5	17.9	322	1	GDC_RAT	P16261 rattus norv
36	276.5	17.9	702	1	CMC1_CAEEL	Q21153 caenorhabd1
37	276	17.8	678	1	UCP5_HUMAN	075746 homo sapien
38	274	17.7	325	1	UCP5_HUMAN	095258 homo sapien
39	265.5	17.2	332	1	GDC_HUMAN	P16260 homo sapien
40	261.5	16.9	675	1	CMC2_HUMAN	09430 homo sapien
41	261	16.9	310	1	ODC1_YEAST	003028 saccharomyc
42	257.5	16.6	315	1	MET_HUMAN	09h2d1 homo sapien
43	249.5	16.1	326	1	YE08_SCHPO	013805 schizosacch
44	249	16.1	315	1	SA18_HUMAN	09h1k4 homo sapien
45	249	16.1	324	1	OMC1_YEAST	P32332 saccharomyc

ALIGNMENTS

RESULT 1
ADPT2_HUMAN
ID ADPT2_HUMAN STANDARD: PRT: 298 AA.
AC P05141: 043350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP-ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Murzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
cloning and sequence."
RL J. Biol. Chem. 265:16060-16063(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87166056; PubMed=3031073;
RA Battini R., Ferrarri S., Kaczmarek L., Calabretta B., Chen S.T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
growth-regulated."
RL J. Biol. Chem. 262:4355-4358(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraia R.,
RA Mazzarella R.A., Schlessinger D., Chen E.Y.;
RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX Becker M., Graves T., Ozerky P.;
RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houdsworth J., Altardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL: M57424; AAA51737.1; -
 DR EMBL: J02683; AAA35579.1; -
 DR EMBL: L78810; AAB39266.1; -
 DR EMBL: AC004000; AAB69347.1; -
 DR EMBL: J03591; AAA36749.1; -
 DR PIR: A29132; A29132.
 DR PIR: C28116; C28116.
 DR Genew: HGNC:10991; SLC25A5.
 DR MIM: 300150; -
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCH_CARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 6 6 V -> L (IN REF. 2).
 FT CONFLICT 66 66 G -> E (IN REF. 2).
 FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
 FT CONFLICT 162 162 V -> G (IN REF. 5).
 FT SEQUENCE 298 AA; 32895 MW; F973C3AED92CA9D3 CRC64;

Query Match 99.4%; Score 1537; DB 1; Length 298;
 Best Local Similarity 99.3%; Pred. No. 9.4e-130;
 Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTPAALSFAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKOYKGIIDCVR 60
 DB 1 MTPAALSFAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKOYKGIIDCVR 60
 QY 61 IPKEOVLSTFWRGNLANVIRYPTQALNFAFKYKQIFLGVDKRTQFRYFAGNLAAG 120
 DB 61 IPKEOVLSTFWRGNLANVIRYPTQALNFAFKYKQIFLGVDKRTQFRYFAGNLAAG 120
 QY 121 GAAGATSLCFVYPLDFARTRLAADVAGKAGAREFERGLGDLVYIKSDGKGLYQGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLAADVAGKAGAREFERGLGDLVYIKSDGKGLYQGFNVS 180
 QY 181 VGGIIIRAAVFGIYDTAKMLDPKNTHTIVISMTAQYTAAGLTSYFEDVRRMM 240
 DB 181 VGGIIIRAAVFGIYDTAKMLDPKNTHTIVISMTAQYTAAGLTSYFEDVRRMM 240
 QY 241 QSGRKGDIVYTGTLDCWKRIARDEGKAFKAGMSNVLMGAGAVLVLYDEIKKYYT 298
 DB 241 QSGRKGDIVYTGTLDCWKRIARDEGKAFKAGMSNVLMGAGAVLVLYDEIKKYYT 298

RESULT 2
 ADT2_RAT
 ID ADT2_RAT STANDARD; PRT; 298 AA.
 AC 009073;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 DE (Adenine nucleotide translocator 2) (ANT 2).
 GN SLC25A5 OR ANT2.

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shinohara Y., Kamida M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RT encoding rat mitochondrial adenine nucleotide translocator.";
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
 CC SKELETAL MUSCLE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL: D12771; BAA02238.1; -
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCH_CARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT SEQUENCE 298 AA; 32901 MW; 6A59204B987E9E35 CRC64;

Query Match 98.6%; Score 1525; DB 1; Length 298;
 Best Local Similarity 98.3%; Pred. No. 1.1e-128;
 Matches 293; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTPAALSFAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKOYKGIIDCVR 60
 DB 1 MTPAALSFAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKOYKGIIDCVR 60
 QY 61 IPKEOVLSTFWRGNLANVIRYPTQALNFAFKYKQIFLGVDKRTQFRYFAGNLAAG 120
 DB 61 IPKEOVLSTFWRGNLANVIRYPTQALNFAFKYKQIFLGVDKRTQFRYFAGNLAAG 120
 QY 121 GAAGATSLCFVYPLDFARTRLAADVAGKAGAREFERGLGDLVYIKSDGKGLYQGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLAADVAGKAGAREFERGLGDLVYIKSDGKGLYQGFNVS 180
 QY 181 VGGIIIRAAVFGIYDTAKMLDPKNTHTIVISMTAQYTAAGLTSYFEDVRRMM 240
 DB 181 VGGIIIRAAVFGIYDTAKMLDPKNTHTIVISMTAQYTAAGLTSYFEDVRRMM 240
 QY 241 QSGRKGDIVYTGTLDCWKRIARDEGKAFKAGMSNVLMGAGAVLVLYDEIKKYYT 298
 DB 241 QSGRKGDIVYTGTLDCWKRIARDEGKAFKAGMSNVLMGAGAVLVLYDEIKKYYT 298

```

RESULT 3
ADP2_MOUSE STANDARD: PRT: 298 AA.
ID ADP2_MOUSE STANDARD: PRT: 298 AA.
AC P51881; Q61311;
DR 01-OCT-1996 (Rel. 34, Created)
DR 01-OCT-1996 (Rel. 34, Last sequence update)
DR 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
GN (Adenine nucleotide translocator 2) (ANT 2).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
RT homologs.";
RL Mamm. Genome 7:25-30(1996).
RN [2]
RC SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Sheldon J.G.;
RL Thesis (1995), University of Cambridge, U.K.
RN [3]
RC SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA Costet P., Laplace C.;
RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
RN [4]
RC REVISIONS.
RA Laplace C.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RC SEQUENCE FROM N.A.
RX MEDLINE=20432087; PubMed=10974536;
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide
RT translocase 1 and 2 genes.";
RL Gene 254:57-66(2000).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U27316; AAC52838.1; -.
DR EMBL: U10404; AAA19009.1; -.
DR EMBL: X70847; CA50196.1; -.
DR EMBL: AF240003; AAF6447.1; -.
DR MGI: MGI:1353496; Slc25a5.
DR InterPro: IPR002067; MLC_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr.3.
DR PRINTS: PR000926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER.3.
KM Mitochondrion, inner membrane; Repeat; Transmembrane; Transport;
FT Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).

```

```

FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32931 MW; 0798E04B987EFEE20 CRC64;

Query Match 98.2%; Score 1519; DB 1; Length 298;
Best Local Similarity 98.0%; Pred. No.3-8e-128;
Matches 292; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTDALSPKDFLAGVAAAIKSTAVAPLERKLLQVHASKQTADKQYGIIDCYVR 60
DB 1 MTDAAVSFAKDFLAGVAAAIKSTAVAPLERKLLQVHASKQTADKQYGIIDCYVR 60
QY 61 IPKEGVLSFWGNNLANVIRFPTQALNFAFKDKYKQIFLGVDKRTQPMRFAGNLSG 120
DB 61 IPKEGVLSFWGNNLANVIRFPTQALNFAFKDKYKQIFLGVDKRTQPMRFAGNLSG 120
QY 121 GAAGATSLCFVYPLDFARTLADYKAGAEERFGIDCLVKIKYSDGIRKGLYGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTLADYKAGAEERFGIDCLVKIKYSDGIRKGLYGFNVS 180
QY 181 VGGIIIRAAFGIYDTAKGLPDPKNTNIVISMTAQTVAAGLTSYPTDPTVRRMM 240
DB 181 VGGIIIRAAFGIYDTAKGLPDPKNTNIVISMTAQTVAAGLTSYPTDPTVRRMM 240
QY 241 QSGRGTDTIMYGTLDCKWKIARDGSKAFEGKAMSNVIRGSGAFVLVLYEIRKKT 298
DB 241 QSGRGTDTIMYGTLDCKWKIARDGSKAFEGKAMSNVIRGSGAFVLVLYEIRKKT 298

RESULT 4
ADP3_BOVIN STANDARD: PRT: 298 AA.
ID ADP3_BOVIN STANDARD: PRT: 298 AA.
AC P32007;
DR 01-JUL-1993 (Rel. 26, Created)
DR 01-JUL-1993 (Rel. 26, Last sequence update)
DR 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine
DE nucleotide translocator 3) (ANT 3).
GN SLc25a6 OR ANT3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=89229093; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues.";
RL Biochemistry 28:866-873(1989).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----

```

DR EMBL: M24103; AAA30769.1; -.
DR PIR: B43646; B43646.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCH_CARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 2 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32877 MW; 1C34E7DF6EDE4061 CRC64;

Query Match 94.2%; Score 1458; DB 1; Length 298;
Best Local Similarity 92.9%; Pred. No. 1e-122;
Matches 274; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTDALSFADFLAGVAAAIKTAAPVIRVKLLQVHASKOITADKQYKGIIDCVYR 60
DB 1 MTEGAISFADFLAGVAAAIKTAAPVIRVKLLQVHASKOITADKQYKGIIDCVYR 60
QY 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASG 120
DB 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASG 120
QY 121 GAAATSLCEFYPLDFAFRTADLVGKAGAREFRGLGDCLVKTKSDGKIGLYOGFNVS 180
DB 121 GAAATSLCEFYPLDFAFRTADLVGKAGAREFRGLGDCLVKTKSDGKIGLYOGFNVS 180
QY 181 VQGIITRAAFEGLYDRAKGMILPDKNTHYISMMIAQTVAVAGVSYPDYVRRRMM 240
DB 181 VQGIITRAAFEGLYDRAKGMILPDKNTHYISMMIAQTVAVAGVSYPDYVRRRMM 240
QY 241 QSGRRKGDIMYTGTLDCWRKTADEGKAPFKGAMSNVLRMGGAFAVLVLDKIK 296
DB 241 QSGRRKGDIMYTGTLDCWRKTADEGKAPFKGAMSNVLRMGGAFAVLVLDKIK 296

RESULT 5
ADT3_HUMAN STANDARD; PRT; 298 AA.
ID ADT3_HUMAN STANDARD; PRT; 298 AA.
AC P12236; Q96C49.
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
DE (Adenine nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=89236396; Pubmed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
ADP/ATP translocase";
RL J. Mol. Biol. 206:261-280(1989).
RN 121
RP SEQUENCE FROM N.A.
RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
RA Margolin J.F.;
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
RN 131
RP SEQUENCE FROM N.A.

RC TISSUE=Brain, Cervix, Eye, and Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
RN 141
RP SEQUENCE OF 36-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; Pubmed=2829183;
RA Houldsworth J., Altardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
level in adult human liver";
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@sib-sib.ch).
CC
DR EMBL: J03592; AAA36750.1; -.
DR EMBL: AY007135; AAG01998.1; -.
DR EMBL: BC007295; AAH07295.1; -.
DR EMBL: BC007850; AAH07850.1; -.
DR EMBL: BC008737; AAH08737.1; -.
DR EMBL: BC008935; AAH08935.1; -.
DR EMBL: BC014775; AAH14775.1; -.
DR PIR: S03894; S03894.
DR PIR: B28116; B28116.
DR Genew: HGNC:10992; SLC25A6.
DR MIM: 300151; -.
DR MIM: 403000; -.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCH_CARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 100 1.
FT REPEAT 101 208 2.
FT REPEAT 209 298 3.
FT REPEAT 209 298 3.
FT CONFLICT 105 108 KHNQ -> RHA (IN REF. 4).
FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
SQ SEQUENCE 298 AA; 32866 MW; 18534E9F0E49672F CRC64;

Query Match 94.0%; Score 1454; DB 1; Length 298;
Best Local Similarity 92.6%; Pred. No. 2.3e-122;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDALSFADFLAGVAAAIKTAAPVIRVKLLQVHASKOITADKQYKGIIDCVYR 60
DB 1 MTEGAISFADFLAGVAAAIKTAAPVIRVKLLQVHASKOITADKQYKGIIDCVYR 60
QY 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASG 120
DB 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASG 120
QY 121 GAAATSLCEFYPLDFAFRTADLVGKAGAREFRGLGDCLVKTKSDGKIGLYOGFNVS 180
DB 121 GAAATSLCEFYPLDFAFRTADLVGKAGAREFRGLGDCLVKTKSDGKIGLYOGFNVS 180

Db 121 GAAGATSLCFVYPLDFAPRLADYGVKSGTEREFGDGLVCKITKSDCIRGLYOGFSVS 180
QY 181 VGGIIIRAAVFGYVDTAKGMLPDPKNTIHVISMIAQVTAVAGLTSPEDTVRRMM 240
Db 181 VGGIIIRAAVFGYVDTAKGMLPDPKNTIHVISMIAQVTAVAGLTSPEDTVRRMM 240
QY 241 OSGRKGTDMYGTGLDCMRKRIARDEGKAFKFGAMSNVLRGAGAVLVLYDEIKY 296
Db 241 OSGRKGTDMYGTGLDCMRKRIARDEGKAFKFGAMSNVLRGAGAVLVLYDEIKY 296
RESULT 6
ADTL_MOUSE
ID ADTL_MOUSE STANDARD: PRT: 298 AA.
AC P48962; 062164;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE ADP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (MANC1).
GN SLC25A4 OR ANT1 OR ANCL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudoautosomal genes and their mouse homologs.";
RL Mann. Genome 7:25-30(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Muscle;
RA Laplace C., Costet P.;
RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes.";
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
CC -----
CC EMBL; U27315; AAC52837.1; -;
CC EMBL; X74510; CA552616.1; -;
CC EMBL; AF240002; AAF64470.1; -;
CC EMBL; BC003791; AAH03791.1; -;
CC EMBL; BC026925; AAH26925.1; -;
CC MGI; MGI:1353495; SLC25A4.
CC InterPro; IPR002067; MLC_carrier.
CC InterPro; IPR001993; Mitoch_carrier.

DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport; Multigene family.
FT TRANSMEM 12 29. 1 (POTENTIAL).
FT TRANSMEM 73 91. 2 (POTENTIAL).
FT TRANSMEM 117 134. 3 (POTENTIAL).
FT TRANSMEM 176 195. 4 (POTENTIAL).
FT TRANSMEM 214 231. 5 (POTENTIAL).
FT TRANSMEM 273 291. 6 (POTENTIAL).
FT REPEAT 1 110. 1.
FT REPEAT 111 208. 2.
FT REPEAT 209 298. 3.
FT CONFLICT 136 136 F -> L (IN REF. 1).
SQ SEQUENCE 298 AA; 32904 MM; 3A849FEAB0981462 CRC64;
Query Match 91.6%; Score 1417; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 4.7e-119; Indels 0; Gaps 0;
Matches 266; Conservative 15; Mismatches 16;
QY 1 MTDALSFADKFLAGVAAAIKSTAVAPIERYKLLQVGHASKQITADKQYGIIDCVVR 60
Db 1 MGDQALSLFKDPLAGIAAASKTAVAPIERYKLLQVGHASKQIAEKQYGIIDCVVR 60
QY 61 IREDEVLSFWRGNLANVIRPEPTQALNFAFDKTKQITFLGVGDKRTQWRIFAGNLASG 120
Db 61 IREDEVLSFWRGNLANVIRPEPTQALNFAFDKTKQITFLGVGDKRTQWRIFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFAPRLADYGVKSGTEREFGDGLVCKITKSDCIRGLYOGFSVS 180
Db 121 GAAGATSLCFVYPLDFAPRLADYGVKSGTEREFGDGLVCKITKSDCIRGLYOGFSVS 180
QY 181 VGGIIIRAAVFGYVDTAKGMLPDPKNTIHVISMIAQVTAVAGLTSPEDTVRRMM 240
Db 181 VGGIIIRAAVFGYVDTAKGMLPDPKNTIHVISMIAQVTAVAGLTSPEDTVRRMM 240
QY 241 OSGRKGTDMYGTGLDCMRKRIARDEGKAFKFGAMSNVLRGAGAVLVLYDEIKY 297
Db 241 OSGRKGTDMYGTGLDCMRKRIARDEGKAFKFGAMSNVLRGAGAVLVLYDEIKY 297
RESULT 7
ADTL_RAT
ID ADTL_RAT STANDARD: PRT: 298 AA.
AC Q05962;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shiohara Y., Kamada M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone encoding rat mitochondrial adenine nucleotide translocator.";
RL Biochim. Biophys. Acta 1152:192-196(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER EXTENT, IN BRAIN AND KIDNEY.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X61667; CAA43842.1; -
DR EMBL: D12770; BAA02237.1; -
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32989 MW; 66704FE78C6BC320 CRC64;
Query Match 91.6%; Score 1417; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 4.7e-119;
Matches 266; Conservative 16; Mismatches 15; Indels 0; Gaps 0;
QY 1 MTDALSFARDFLAGVAAAIKSTAVAPIERVKLLLOVONHASKQITPAKQYGIIDCVVR 60
DB 1 MGDAALSFLEDFLAGVAAAIKSTAVAPIERVKLLLOVONHASKQISAEKQYGIIDCVVR 60
QY 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLSAG 120
DB 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLSAG 120
QY 121 GAAGATSLCEVYPLDPAFRTIADLVGKAGARERGGLDCLVTKYKSDIGIKGLQGFNV 180
DB 121 GAAGATSLCEVYPLDPAFRTIADLVGKAGARERGGLDCLVTKYKSDIGIKGLQGFNV 180
QY 181 VQGIITRAAFYFGYIDPAKGLPDPKNTNHYISWIAQTVAVAGLSYPTDVRRRMM 240
DB 181 VQGIITRAAFYFGYIDPAKGLPDPKNTNHYISWIAQTVAVAGLSYPTDVRRRMM 240
QY 241 QSGRKGFDIMYTGTLDCWRKIARDGSKAFKFGAMSNVLRMGGAFFVLVYDEIKKY 297
DB 241 QSGRKGFDIMYTGTLDCWRKIARDGSKAFKFGAMSNVLRMGGAFFVLVYDEIKKY 297
RESULT 8
ADTL_BOVIN STANDARD; PRT; 297 AA.
ID ADTL_BOVIN
AC P02722;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, heart isoform T1 (ADP/ATP translocase 1)
DE (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86229093; PubMed=2540808;
* Powell S.J., Mead S.M., Runswick M.J., Walker J.E.;

```

```

RT "two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues.";
RL Biochemistry 28:866-873(1989).
RN [2]
RP SEQUENCE
RX MEDLINE=82186267; PubMed=7076130;
RA Aquila H., Mistr D., Eulitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
RT mitochondria.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
RN [3]
RP SEQUENCE OF 207-297 FROM N.A.
RX MEDLINE=86295775; PubMed=3017341;
RA Rasmussen U.B., Wohlrab H.;
RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
RT an unusually short 3'-noncoding sequence.";
RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M13783; AAA30363.1; -
DR EMBL: M24102; AAA30768.1; -
DR PIR: A03181; XMO.
DR PIR: A24822; A24822.
DR PIR: A43646; A43646.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family; Methylation.
FT INT_MET 0 0
FT MOD_RES 1 1 BLOCKED.
FT MOD_RES 51 51 METHYLATION (POTENTIAL).
FT TRANSMEM 11 28 1 (POTENTIAL).
FT TRANSMEM 72 90 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 175 194 4 (POTENTIAL).
FT TRANSMEM 213 230 5 (POTENTIAL).
FT TRANSMEM 272 290 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40AE848 CRC64;
Query Match 91.4%; Score 1414; DB 1; Length 297;
Best Local Similarity 89.9%; Pred. No. 8.6e-119;
Matches 266; Conservative 16; Mismatches 14; Indels 0; Gaps 0;
QY 2 TDAALSFARDFLAGVAAAIKSTAVAPIERVKLLLOVONHASKQITPAKQYGIIDCVVR 61
DB 1 SDQALSFLEDFLAGVAAAIKSTAVAPIERVKLLLOVONHASKQISAEKQYGIIDCVVR 60
QY 62 PKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLSAG 121
DB 62 PKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLSAG 120
QY 122 AAGATSLCEVYPLDPAFRTIADLVGKAGARERGGLDCLVTKYKSDIGIKGLQGFNV 181
DB 122 AAGATSLCEVYPLDPAFRTIADLVGKAGARERGGLDCLVTKYKSDIGIKGLQGFNV 181

```

DB 121 AAGATSLCFVYPLDPAFRLADVGKGAQREFGLGNCITKIFKSDGLRGLYQGFNVSV 180
 QY 182 0GIIITTYRAAYFGIYDTAKGMLDPKPNTHIVISMIAQVTAAGLTSTFFTVRRRMNQ 241
 DB 181 0GIIITTYRAAYFGIYDTAKGMLDPKPNTHIVISMIAQVTAAGLTSTFFTVRRRMNQ 240
 QY 242 SRRKGTDMITVTGTLGCMRKRIARDEGKAFKFGKAMSVNLGKMGAFVLYYDEIKKY 297
 DB 241 SRRKADIMVTGTVCCWKRIANDEGPKAFKFGKAMSVNLGKMGAFVLYYDEIKKF 296

RESULT 9
 ADT1_HUMAN
 ID ADT1_HUMAN STANDARD: PRT: 298 AA.
 AC P12235;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 GN SLC25A4 OR ANT1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89236396; PubMed=2541251;
 RA Cozens A.L., Runswick M.J., Walker J.E.;
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.";
 RL J. Mol. Biol. 206:261-280(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89340499; PubMed=2547778;
 RA Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J., Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
 RT "A human muscle adenine nucleotide translocator gene has four exons, is located on chromosome 4, and is differentially expressed.";
 RL J. Biol. Chem. 264:13996-14004(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88041149; PubMed=2823266;
 RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
 RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader peptide, divergence from a fibroblast translocator cDNA, and coevolution with mitochondrial DNA genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Eye;
 RA Strausberg R.;
 RT Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1-37 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Attard J.G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 RN [6]
 RP VARIANTS PEO PRO-114 AND MET-289
 RX MEDLINE=20385067; PubMed=10926541;
 RA Kaumonen J., Juselius J.K., Tiliant V., Kytala A., Zeviani M., Cont G.P., Keinanen J., Peltonen L., Suomalainen A.;
 RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";
 RL Science 289:782-785(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant progressive external ophthalmoplegia with various mitochondrial DNA deletions (PEO). Patients with PEO have mitochondrial myopathy, progressive external ophthalmoplegia, and other abnormalities associated with multiple different deletions of mitochondrial DNA.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J02966; AAA61223.1; -;
 DR EMBL: J03593; AAA36751.1; -;
 DR EMBL: J04982; AAA51736.1; -;
 DR EMBL: BC008664; AAH08664.1; -;
 DR PIR: A28116; A28116.
 DR PIR: A39891; A39891.
 DR PIR: S03893; S03893.
 DR PIR: A44778; A44778.
 DR GeneW: HGNC:10990; SLC25A4.
 DR MIM: 103220; -;
 DR MIM: 157640; -;
 DR InterPro: IPR002067; MLC carrier.
 DR InterPro: IPR001993; Mitoch carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family; Disease mutation.
 FT TRANSMEM 12 29
 FT TRANSMEM 73 91 1 (POTENTIAL).
 FT TRANSMEM 117 134 2 (POTENTIAL).
 FT TRANSMEM 176 195 3 (POTENTIAL).
 FT TRANSMEM 214 231 4 (POTENTIAL).
 FT TRANSMEM 273 291 5 (POTENTIAL).
 FT REPEAT 1 110 6 (POTENTIAL).
 FT REPEAT 111 208 1.
 FT REPEAT 209 298 2.
 FT VARIANT 114 114 3.
 FT VARIANT 289 289 A -> P (IN PEO).
 FT VARIANT /FTID=VAR_012111.
 FT VARIANT /FTID=VAR_012112.
 FT CONFLICT 16 16 G -> A (IN REF. 3).
 FT CONFLICT 147 149 V -> L (IN REF. 3).
 FT CONFLICT 227 227 KGA -> RR (IN REF. 3).
 FT CONFLICT 227 227 V -> L (IN REF. 3).
 SQ SEQUENCE 298 AA: 33064 MW: 59PDPFACETGCFBB CRC64;
 Query Match 91.3%: Score 1413; DB 1; Length 298;
 Best Local Similarity 89.2%: Pred No. 1, 1e-118;
 Matches 265; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTDAAISFAKDELAVGAAIAISKTAVALPIERKLLQVOHASKQITADKQYGIIDCVVR 60
 DB 1 MCDHAWSLFKDLFLAGVAAVASKTAVAPIERKLLQVOHASKQISAEKQYGIIDCVVR 60
 QY 61 IRKEDEVLSEFWRGNLAVNRYRPTQALNFAFDKRYKQITLGVGDKTKTQWRPFAGLWAG 120
 DB 61 IRKEDEVLSEFWRGNLAVNRYRPTQALNFAFDKRYKQITLGVGDKTKTQWRPFAGLWAG 120
 QY 121 GAAGATSLCFVYPLDPAFRLADVGKGAQREFGLGNCITKIFKSDGLRGLYQGFNVSV 180
 DB 121 GAAGATSLCFVYPLDPAFRLADVGKGAQREFGLGNCITKIFKSDGLRGLYQGFNVSV 180
 QY 181 VOGIIITTYRAAYFGIYDTAKGMLDPKPNTHIVISMIAQVTAAGLTSTFFTVRRRMNQ 240
 DB 181 VOGIIITTYRAAYFGIYDTAKGMLDPKPNTHIVISMIAQVTAAGLTSTFFTVRRRMNQ 240

```

OY 241 OSGRKGTDIMYTGTLDCMRKIADEGKAFKAGMSVNLKMGAFVLYLVYDEIKKY 297
DB 241 OSGRKGADIMYTGTCDCMRKIADEGKAFKAGMSVNLKMGAFVLYLVYDEIKKY 297

RESULT 10
ADT_DROME STANDARD; PRT; 297 AA.
AC Q26365; Q26254; P91614; O9V270;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
translocator) (ANT) (Stress sensitive B protein).
GN SSB OR A/A-T OR CG16944.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_taxid=7227;
RN RP SEQUENCE FROM N.A.
RX MEDLINE=92389367; Pubmed=1387687;
RA Louvi A., Tsiftlidou S.G.;
RT "A cDNA clone encoding the ADP/ATP translocase of Drosophila
melanogaster shows a high degree of similarity with the mammalian
ADP/ATP translocases."
RL J. Mol. Evol. 35:44-50(1992).
RN RP SEQUENCE FROM N.A.
RX MEDLINE=94350065; Pubmed=7520869;
RA Hutter P., Karch F.;
RT "Molecular analysis of a candidate gene for the reproductive
isolation between sibling species of Drosophila."
RL Experientia 50:749-762(1994).
RN RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Morten J.R., Vandeil M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Peiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Adair J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Bailly R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkov D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
Foster K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Klaiman B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkllov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson W., Skupski M.P., Smith T.,

```

```

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane (By similarity).
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S43651; AAB3114.1; -
DR EMBL; S71762; AAB31734.3; -
DR EMBL; Y10618; CAA71628.1; -
DR EMBL; AEO03484; AAF47957.1; -
DR FlyBase; FBgn0003360; ssb.
DR InterPro; IPR002067; MLC_carrier.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 14 31 1 (POTENTIAL).
FT TRANSMEM 75 93 2 (POTENTIAL).
FT TRANSMEM 119 136 3 (POTENTIAL).
FT TRANSMEM 177 196 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 272 290 6 (POTENTIAL).
FT TRANSMEM 18 19 QV -> GI (IN REF. 3 AND 4).
FT CONFLICT 81 81 I -> Y (IN REF. 1).
FT CONFLICT 200 200 R -> RG (IN REF. 3 AND 4).
FT CONFLICT 266 266 R -> A (IN REF. 2).
FT CONFLICT 267 268 PC -> TGA (IN REF. 3 AND 4).
FT CONFLICT 268 268 C -> S (IN REF. 1).
SQ SEQUENCE 297 AA; 32880 MW; AA639439986F9750 CRC64;

Query Match 78.8%; Score 1218.5; DB 1; Length 297;
Best Local Similarity 80.5%; Pred. No. 2.3e-101;
Matches 235; Conservative 20; Mismatches 34; Indels 3; Gaps 3;

```

```

RESULT 11
ADT_ANOGA STANDARD: PRT: 301 AA.
ID ADT_ANOGA
AC Q27238;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
translocator) (ANT).
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
OC Culicoides; Anophelinae.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G3;
RX MEDLINE=94348635; PubMed=8069414;
RA Beard C.B., Crews-Oyen A.E., Kumar V.K., Collins F.H.;
RT "A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles
gambiae."
RL Insect Mol. Biol. 3:35-40(1994).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sdb.ch/announce/
or send an email to license@sdb-sdb.ch).
-----
CC EMBL: L11618; AAB04104.1; -.
CC EMBL: L11617; AAB04105.1; -.
CC InterPro: IPR002067; Mlt_carrier.
CC InterPro: IPR001993; Mitoch_carrier.
CC Pfam: PF00153; mito_carr; 3.
CC PRINTS: PR00926; MITOCARRIER.
CC PROSITE: PS00215; MITOCH_CARRIER; 3.
CC Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport.
CC TRANSMEM 14 31 1 (POTENTIAL).
CC TRANSMEM 75 93 2 (POTENTIAL).
CC TRANSMEM 119 136 3 (POTENTIAL).
CC TRANSMEM 178 197 4 (POTENTIAL).
CC TRANSMEM 216 233 5 (POTENTIAL).
CC TRANSMEM 275 293 6 (POTENTIAL).
CC TRANSMEM 301 AA; 32863 MW; 4CC9EL7C9F8DA08B CRC64;
SQ SEQUENCE
Query Match 76.9%; Score 1190; DB 1; Length 301;
Best Local Similarity 78.8%; Pred. No. 8e-99;
Matches 227; Conservative 18; Mismatches 43; Indels 0; Gaps 0;

```

```

DB 190 RAAIFGCEPTAGKMLPDPKNTSIFVSMALAOVYTTASGLISPEFDVRRMMMQSPKCS 249
||||| :|||||
OY 248 DIMYGTGLDCKWKRIARDEGGKAFKFGAMSVMVLGKMGAFVLYDEIK 295
::|| ||||| : || |||||
DB 250 EVMYKNTLDCKVWKIGKQSGCAFFKGAFSNVLRGTGALVLYFDEVK 297
||||| :|||||
RESULT 12
ADT_CHLKE STANDARD: PRT: 339 AA.
ID ADT_CHLKE
AC P31692;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
translocator) (ANT).
OS Chlorella kessleri.
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
OC Chlorellaceae; Chlorella.
OX NCBI_TaxID=3074;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92084708; PubMed=1748677;
RA Hilgarch C., Sauer N., Tanner W.;
RT "Glucose increases the expression of the ATP/ADP translocator and the
glyceralddehyde-3-phosphate dehydrogenase genes in Chlorella."
RL J. Biol. Chem. 266:24044-24047(1991).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sdb.ch/announce/
or send an email to license@sdb-sdb.ch).
-----
CC EMBL: M76669; AA33027.1; -.
CC PIR: A41677; A41677.
CC InterPro: IPR002067; Mlt_carrier.
CC InterPro: IPR001993; Mitoch_carrier.
CC Pfam: PF00153; mito_carr; 3.
CC PRINTS: PR00926; MITOCARRIER.
CC PROSITE: PS00215; MITOCH_CARRIER; 3.
CC Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport.
CC TRANSMEM 45 62 1 (POTENTIAL).
CC TRANSMEM 108 126 2 (POTENTIAL).
CC TRANSMEM 151 168 3 (POTENTIAL).
CC TRANSMEM 209 228 4 (POTENTIAL).
CC TRANSMEM 248 265 5 (POTENTIAL).
CC TRANSMEM 304 322 6 (POTENTIAL).
CC TRANSMEM 339 AA; 36686 MW; 54779734A3B3942 CRC64;
SQ SEQUENCE
Query Match 62.6%; Score 968; DB 1; Length 339;
Best Local Similarity 65.8%; Pred. No. 5.6e-79;
Matches 194; Conservative 29; Mismatches 64; Indels 8; Gaps 5;

```

```

Db 158 GAGSLIVPLDFAKRLADVG-SGKSREFTGLVDLSKVKRGPMALVQGVSVQ 216
QY 184 IIVRAAYFGIYDPAKML-PDPKNTHTIVSMIAQVTAVAGLTSYPPDVTVRMM 242
Db 217 IIVRGAYFGIYDPAKMLERDEKNTANFPAKMAVAQAVTAGAGLSTPFDVTVRMM 276
QY 243 GRKGTDMITGTLDCKMKRIARDEGKAFFKAGMSNVLKMGAFVLYLDEIRKY 297
Db 277 ---GGEROYNGTIDCMRKVAQOEGMKAFKAGMSNVLKMGAFVLYLDEIRKY 328

RESULT 13
ADT1_GOSHI STANDARD; PRT; 386 AA.
ID ADT1_GOSHI STANDARD; PRT; 386 AA.
AC 023342;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein 1, mitochondrial precursor (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN ANTI.
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Texas Marker 1; TISSUE=Fiber;
RA Shin H., Brown R.M. Jr.;
RT "Two cDNA sequences for the adenine nucleotide translocator, CAN1 and CAN2, from cotton fibers (Gossypium hirsutum).";
RL (In) Plant Gene Register PGR97-130.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF006489; AAB72047.1; -
DR InterPro: IPR002067; MitCarrier.
DR InterPro: IPR001993; MitochCarrier.
DR Pfam: PF00153; mito-car; 3.
DR PRINTS: PR00926; MITOCHARRIER.
DR PROSITE: PS00215; MITOCHARRIER. 2.
KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Transit peptide; Multigene family.
FT TRANSIT 1 76 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 1 386 ADP/ATP CARRIER PROTEIN 1.
FT TRANSMEM 90 107 1 (POTENTIAL).
FT TRANSMEM 152 170 2 (POTENTIAL).
FT TRANSMEM 195 212 3 (POTENTIAL).
FT TRANSMEM 256 275 4 (POTENTIAL).
FT TRANSMEM 295 312 5 (POTENTIAL).
FT TRANSMEM 351 369 6 (POTENTIAL).
SQ SEQUENCE 386 AA; 42093 MW; A05F76C73FFED66 CRC64;

Query Match 49.8%; Score 771; DB 1; Length 386;
Best Local Similarity 55.4%; Pred. NO. 2.4e-61;
Matches 165; Conservative 33; Mismatches 79; Indels 22; Gaps 7;
QY 7 SFANDFLAGVAIAIKTAVPIERVKLLQVQ-HASKQITADKQYGIIDCVRIPEEQ 65
Db 85 SFALDFLMGSAVSAVSTAAPRIERVKLLQNDQEMIKSGLSPEYKIGGCFRRTIKDE 144
QY 66 EVLSFMGNLANVIRPEPTQALNFAFKDKYKQITLGGVADKRTQWRIRFAGNLASGAGA 125

```

```

Db 145 GFGSLMKGNTANVIRPEPTQALNFAFKDKYKQITLGGVADKRTQWRIRFAGNLASGAGA 203
QY 126 TSICEFVPLDPAKRLAD--VKGAGAEERERFGIDCLVTKYSKGLYQGVNVSQ 183
Db 204 SSLFVPLSDPAKRLANDAKAKKGGROPNGLVDYRRTKLSKGLYQGVNVSQ 263
QY 184 IIVRAAYFGIYDPAK-----GMLPDPKNTHTIVSMIAQVTAVAGLTSYPPDVTVRMM 238
Db 264 IIVRGAYFGIYDPAKLVLLTSGMQDSEFASVFLGWL-----TNGALASYPIDVTVRMM 319
QY 239 MMSGKGTDMITGTLDCKMKRIARDEGKAFFKAGMSNVLKMGAFVLYLDEIRKY 294
Db 320 MMTSGKA---VKRKSIDPAESQILKNEGKSLFKAGSNILRLAAGAGVLYLDEIRKY 376
QY 295 --KKY 297
Db 377 GKRY 381

RESULT 14
ADT1_SCHPO STANDARD; PRT; 322 AA.
ID ADT1_SCHPO STANDARD; PRT; 322 AA.
AC 009186;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
GN ANCI OR SPBC530.10C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=96257204; PubMed=8675018;
RA Couzin N., Trezguet V., Saux A.L., Lauguin G.J.M.;
RT "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation in Saccharomyces cerevisiae.";
RL Gene 171:113-117(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Soutos J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltham T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volkart G., Aert R., Robben J., Grymptre B., Welteens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritze C., Holzer E., Reinhardt R., Pohl T.M., Borzym K., Langer I., Beck A., Lehnach R., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Sipakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";

```


GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:43:45 ; Search time 25.3617 Seconds

(without alignments)
2421.054 Million cell updates/sec

Title: US-09-393-441-32

Perfect score: 1547
Sequence: 1 MTDALSPAFKDFLAGVAAA.....LNGMGAFVLYLDEIKKTF 298

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

```
SPREMBL.21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_virus:*
16: sp_bacterioplasmid:*
17: sp_archaeoplasmid:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1515	97.9	298	6	08SQH5 bos taurus
2	1446	93.5	298	13	09PRH1 rana rugosa
3	1443	93.3	298	13	09PRH2 rana rugosa
4	1439	93.0	298	13	09YIC4 rana rugosa
5	1425	92.1	298	13	0919M9 xenopus lae
6	1423	92.0	298	6	046373 oryctolagus
7	1417	91.6	298	11	062164 mus musculus
8	1295	83.7	317	13	091336 rana sylvatica
9	1278	82.6	299	5	095VX4 ethiostigmus
10	1253.5	81.0	299	5	095S30 drosophila
11	1248.5	80.7	300	5	09NHWS lucilia cup
12	1190.5	77.0	288	5	044093 drosophila
13	1185.5	76.6	288	5	044094 drosophila
14	1145.5	74.0	304	5	025129 halocynthia
15	1125.5	72.8	307	5	062526 drosophila
16	1102	71.2	315	4	09HOC2 homo sapien

17	1032	66.7	300	5	045865 caenorhabditis
18	1029	66.5	313	5	P91410 caenorhabditis
19	1029	66.5	313	5	021103 caenorhabditis
20	986	63.7	300	5	001813 caenorhabditis
21	985	63.7	309	5	097470 dictyostelium
22	983	63.5	300	5	017407 caenorhabditis
23	950.5	61.4	318	5	09B336 toxoplasma
24	949.5	61.4	307	8	09XM22 ascaris suum
25	939	60.7	301	5	025692 plasmidium
26	938	60.6	301	5	026006 plasmidium
27	819	52.9	170	6	09XS69 sus scrofa
28	778	50.3	305	3	09P8M1 yarrowia
29	759	49.1	326	5	P91270 caenorhabditis
30	755	48.8	303	3	074260 candida par
31	753	48.7	317	5	09N647 leishmania
32	752	48.6	307	5	076286 trypanosoma
33	750	48.5	386	10	P93767 lycopersicon
34	749.5	48.4	306	5	018683 caenorhabditis
35	747	48.3	388	10	049875 lupinus albus
36	746	48.2	306	3	P78754 schizosaccharomyces
37	746	48.2	379	10	049447 arabidopsis
38	745	48.2	307	5	026697 trypanosoma
39	740	47.8	331	10	041628 triticum
40	721.5	46.6	305	3	09P876 pichia
41	718.5	46.4	305	3	09P875 pichia
42	717.5	46.4	308	3	08TFA7 neocallimastix
43	690.5	44.6	300	10	09PFM86 arabidopsis
44	665.5	43.0	298	5	021809 caenorhabditis
45	656.5	42.4	262	10	09AVT6 picea abies

ALIGNMENTS

RESULT 1
ID 08SQH5 PRELIMINARY; PRT; 298 AA.
AC 08SQH5;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adenine nucleotide translocase 2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamazaki N., Shinohara Y., Tanida K., Terada H.;
RT "Structural properties of mammalian mitochondrial ADP/ATP carriers:
RT Identification of possible amino acids that determine functional
RT differences in its isoforms";
RL Mitochondrion 1:371-379(2002).
DR EMBL: AB065433; BAB84673.1; -
SQ SEQUENCE 298 AA; 32955 MW; CB6897BB987B79C0 CRC64;

Query Match 97.9%; Score 1515; DB 6; Length 298;
Best local similarity 97.7%; Pred. No. 4.8e-126;
Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY	1	MTDALSPAFKDFLAGVAAAIKRAVAPRIERVKLLLOVHASKRITADKQYKGIIDCVR	60
DB	1	MTDALSPAFKDFLAGVAAAIKRAVAPRIERVKLLLOVHASKRITADKQYKGIIDCVR	60
QY	61	IPKXOEVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKPTQFMYFAGNLASG	120
DB	61	IPKXOGVLSFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKPTQFMYFAGNLASG	120
QY	121	GAAGATSLCFYVPLDFKARTLADVGKAGAREPRGLGDCLVKTKDGKGLQGPNV	180
DB	121	GAAGATSLCFYVPLDFKARTLADVGKAGAREPRGLGDCLVKTKDGKGLQGPNV	180

QY 181 VGGIITRYAAYFGIYDTAGKMLPDPKNTHTIVISWIAQTVAAGLTSYPDVTVRMM 240
 DB 181 VGGIITRYAAYFGIYDTAGKMLPDPKNTHTIVISWIAQTVAAGLTSYPDVTVRMM 240
 CY 241 OSGRGKTDIMYGTLDCKMKIARDGSKAFKFGAMSNTLRGAGAVLVLYDEIKKY 298
 DB 241 OSGRGKTDIMYGTLDCKMKIARDGSKAFKFGAMSNTLRGAGAVLVLYDEIKKY 298

RESULT 2

Q9PRH1 PRELIMINARY: PRT; 298 AA.
 AC Q9PRH1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana rugosa (wrinkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99083429; PubMed=9866197;
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorph sex chromosomes
 of 2, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
 a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AB008463; BAA36513.1; -;
 DR EMBL; AB008456; BAA36508.1; -;
 DR EMBL; AB008461; BAA36511.1; -;
 DR EMBL; AB008462; BAA36512.1; -;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mlt_carrier.
 DR InterPro; IPR002030; Mlt_uncoupling.
 DR Pfam; PF00153; mltc_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

Query Match 93.5%; Score 1446; DB 13; Length 298;
 Best Local Similarity 91.9%; Pred. No. 6, 2e-120;
 Matches 273; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTDALSFAPKDELAGGVAIAISKTAVAPTERYKLLQVGHASKQITADKQYGIIDCV 60
 DB 1 MTDALSFAPKDELAGGVAIAISKTAVAPTERYKLLQVGHASKQITADKQYGIIDCV 60
 QY 61 IRKEDEVLSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQWRYPAGNLASG 120
 DB 61 IRKEDEVLSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPARTRLAADVKGAGREFRGLGDLVKIYKSDGKGLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDPARTRLAADVKGAGREFRGLGDLVKIYKSDGKGLYOGFNVS 180
 QY 181 VGGIITRYAAYFGIYDTAGKMLPDPKNTHTIVISWIAQTVAAGLTSYPDVTVRMM 240
 DB 181 VGGIITRYAAYFGIYDTAGKMLPDPKNTHTIVISWIAQTVAAGLTSYPDVTVRMM 240
 QY 241 OSGRGKTDIMYGTLDCKMKIARDGSKAFKFGAMSNTLRGAGAVLVLYDEIKKY 297
 DB 241 OSGRGKTDIMYGTLDCKMKIARDGSKAFKFGAMSNTLRGAGAVLVLYDEIKKY 297

RESULT 3

Q9PRH2

ID Q9PRH2 PRELIMINARY: PRT; 298 AA.
 AC Q9PRH2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana rugosa (wrinkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99083429; PubMed=9866197;
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorph sex chromosomes
 of 2, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
 a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AB008460; BAA36510.1; -;
 DR EMBL; AB008458; BAA36508.1; -;
 DR EMBL; AB008459; BAA36509.1; -;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mlt_carrier.
 DR InterPro; IPR002030; Mlt_uncoupling.
 DR Pfam; PF00153; mltc_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;

Query Match 93.3%; Score 1443; DB 13; Length 298;
 Best Local Similarity 91.6%; Pred. No. 1, 1e-119;
 Matches 272; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTDALSFAPKDELAGGVAIAISKTAVAPTERYKLLQVGHASKQITADKQYGIIDCV 60
 DB 1 MTDALSFAPKDELAGGVAIAISKTAVAPTERYKLLQVGHASKQITADKQYGIIDCV 60
 QY 61 IRKEDEVLSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQWRYPAGNLASG 120
 DB 61 IRKEDEVLSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQWRYPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPARTRLAADVKGAGREFRGLGDLVKIYKSDGKGLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDPARTRLAADVKGAGREFRGLGDLVKIYKSDGKGLYOGFNVS 180
 QY 181 VGGIITRYAAYFGIYDTAGKMLPDPKNTHTIVISWIAQTVAAGLTSYPDVTVRMM 240
 DB 181 VGGIITRYAAYFGIYDTAGKMLPDPKNTHTIVISWIAQTVAAGLTSYPDVTVRMM 240
 QY 241 OSGRGKTDIMYGTLDCKMKIARDGSKAFKFGAMSNTLRGAGAVLVLYDEIKKY 297
 DB 241 OSGRGKTDIMYGTLDCKMKIARDGSKAFKFGAMSNTLRGAGAVLVLYDEIKKY 297

RESULT 4

Q9YIC4 PRELIMINARY: PRT; 298 AA.
 ID Q9YIC4;
 AC Q9YIC4;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana rugosa (wrinkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.

RA MEDLINE-99083429; PubMed-9866197;
 RA Mura I., Ohnani H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromorphic sex chromosomes
 RT 2, W, X, and Y in the frog *Rana rugosa*, inferred from the sequences of
 RT a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB008457; BAA36507.1;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR002030; Mlt_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA: 33068 MW: 158270ED37099A00 CRC64;

Query Match 93.0%; Score 1439; DB 13; Length 298;
 Best Local Similarity 91.2%; Pred. No. 2,6e-119;
 Matches 271; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

OY 1 MTDALSFADKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQTADKQYGIIDCVVR 60
 DB 1 MTDALISFAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQTADKQYGIIDCVVR 60
 OY 61 IPKEDEVLSPFMRGNLANVIRFPTQALNFAFDKQYKQIFLAGVDKRTQFWRFPAGNLASG 120
 DB 61 IPKEGDFVSPFMRGNLANVIRFPTQALNFAFDKQYKQIFLDVNDKRTQFWRFPAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFAPTRLAADYKAGAREFRIGDCLVKIKYKSDGKLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFAPTRLAADYKAGAREFRIGDCLVKIKYKSDGKLYOGFNVS 180
 OY 181 VOGIIIRAAVFGIYDTAKGMLPDPKNTHTIVSMIAQVTAVAGLTSTYPTVRRMM 240
 DB 181 VOGIIIRAAVFGIYDTAKGMLPDPKNTHTIVSMIAQVTAVAGLTSTYPTVRRMM 240
 OY 241 OSGRKGTDMVTGTLDCWKRIARDEGSKAFKFGANSNVLRGMGAFVLVLYEIKY 297
 DB 241 OSGRKGAELMVSGLTIDCWKRIARDEGSKAFKFGANSNVLRGMGAFVLVLYDELK 297

RESULT 5

O919M9 PRELIMINARY; PRT: 298 AA.

ID O919M9
 AC O919M9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Adenine nucleotide translocase.
 GN AN1.
 OS *Xenopus laevis* (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Xenopodine; *Xenopus*.
 OX NCBI_TaxID=8353;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversage R.A.;
 RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
 RT Dynamic Patterns of Expression During Development.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF213147; AAF64471.1;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR002030; Mlt_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.

DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA: 32940 MW: 918740133751877F CRC64;

Query Match 92.1%; Score 1425; DB 13; Length 298;
 Best Local Similarity 91.6%; Pred. No. 4,5e-118;
 Matches 271; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

OY 1 MTDALSFADKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQTADKQYGIIDCVVR 60
 DB 1 MTDALISFAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQTADKQYGIIDCVVR 60
 OY 61 IPKEDEVLSPFMRGNLANVIRFPTQALNFAFDKQYKQIFLAGVDKRTQFWRFPAGNLASG 120
 DB 61 IPKEGDFVSPFMRGNLANVIRFPTQALNFAFDKQYKQIFLDVNDKRTQFWRFPAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFAPTRLAADYKAGAREFRIGDCLVKIKYKSDGKLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFAPTRLAADYKAGAREFRIGDCLVKIKYKSDGKLYOGFNVS 180
 OY 181 VOGIIIRAAVFGIYDTAKGMLPDPKNTHTIVSMIAQVTAVAGLTSTYPTVRRMM 240
 DB 181 VOGIIIRAAVFGIYDTAKGMLPDPKNTHTIVSMIAQVTAVAGLTSTYPTVRRMM 240
 OY 241 OSGRKGTDMVTGTLDCWKRIARDEGSKAFKFGANSNVLRGMGAFVLVLYEIKY 296
 DB 241 OSGRKGAELMVSGLTIDCWKRIARDEGSKAFKFGANSNVLRGMGAFVLVLYDELK 296

RESULT 6

O46373 PRELIMINARY; PRT: 298 AA.

ID O46373
 AC O46373;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ADP/ATP translocase.
 OS *Oryctolagus cuniculus* (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-SKELETAL MUSCLE;
 RA Yamaguchi N., Kasai M.;
 RT "Identification of a 30kDa calsequestrin-binding protein, which
 RT regulates calcium release from sarcoplasmic reticulum of rabbit
 RT skeletal muscle.";
 RL J. Biochem. 335:541-547(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB009386; BAA23777.1;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA: 32901 MW: CAEA32C88164AD78 CRC64;

Query Match 92.0%; Score 1423; DB 6; Length 298;
 Best Local Similarity 89.9%; Pred. No. 6,8e-118;
 Matches 267; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

OY 1 MTDALSFADKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQTADKQYGIIDCVVR 60
 DB 1 MSDQSLFKDPLAGVAAAVKSTAVAPIERVKLLQVOHASKQSAEKQYGIIDCVVR 60
 OY 61 IPKEDEVLSPFMRGNLANVIRFPTQALNFAFDKQYKQIFLAGVDKRTQFWRFPAGNLASG 120
 DB 61 IPKEGDFVSPFMRGNLANVIRFPTQALNFAFDKQYKQIFLDVNDKRTQFWRFPAGNLASG 120

Db	181	VOGIIITRAAFGLITDYPAKAGLPPPKNTHTFVSMIMIAOSTAVAGFGSTFPDITVRRMM	240
Oy	241	QSGRKGTDIMYTGTLDCMKRIADDEGKAFFK	272
Db	241	QSGRKGAEIMYSTGITDCWKIARDEGGNAFFR	272

RESULT	9
095VX4	
ID	095VX4
PRELIMINARY	PR1
299	AA.
AC	095VX4;
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT	01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE	ADP-ATP translocator.
OS	Ethmostigmus rubripes.
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Myriapoda; Chilopoda; Pleurostigmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus
OX	NCBI_TaxID=62613;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Burnell J.N.;
RT	"Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus rubripes.";
RL	Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR	EMBL: AF401758; AA102100.1; --
DR	InterPro: IPR001993; MitoCh_carrier.
DR	Pfam: PF00153; mito_carri_3.
DR	PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_2.
QO	SEQUENCE 299 AA; 33037 MW; 3C3BBC26E7C305E CRC64;

Query Match	82.6%	Score 1278	DB 5	Length 259
Best Local Similarity	82.8%	Pred. No. 4.7e105		
Matches 241	Conservative 22	Mismatches 0	Indels 0	Gaps 0

QY	5	ALSAPEKDIAGVAAASIKSTVAIERKLLQVHASKOTAPKQYKGIIDCVYRIPE	64
Db	5	AVSLFKDPIAGVAAASIKSTVAIERKLLQVHASKOTAPKQYKGIIDCVYRIPE	64
QY	65	QEVLSFMWGNLANIYRFYPTQALNFAEKDKYQIIFLGVDKRIQFWRYFAGNLASGGAAG	124
Db	65	QGIISYMGNGLANIYRFYPTQALNFAEKDKYQIIFLGVDKRIQFWRYFAGNLASGGAAG	124
QY	125	ATSLCFVYPLDEARTRLAADYDKAGAREEPFGIDCLVTKYIKSGICIGLVQGEVNSVQGI	184
Db	125	ATSLCFVYPLFAFTRILAADIGKLEBQREFPGIDCLVTKYIKSGICIGLVTRGFEVNSVQGI	184
QY	185	IIVRAAYFGIDTAKGMLPDKRNTHIYISWMIADTVAVNAGLTSYFPEDTVRRMMMSGR	244
Db	185	IIVRAAYFGTVDFAKGMPLPDKRNPIYISMLIAQTVTTCAGIISYFPEDTVRRMMMSGR	244
QY	245	KGTIDMTGTLIDCKRRKARADSGAARFKGANSNVLRMGCAFVLYLDEIK	295
Db	245	KKAIDILKNNTIDCKGKIYKTEGGAARFKGAFSNLIRGGSFVLYLDEIK	295

RESULT 10		
Q95530		
ID	Q95530	PRELIMINARY;
AC	Q95530;	PRT; 299 AA.
DT	01-DEC-2001 (TrEMBLrel. 19, Created)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)	
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)	
DE	GM12886p (LP02726p).	
GN	SESB OR CG16944.	
OS	Drosophila melanogaster (Fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Ephyroidae; Drosophilidae; Drosophila.	
OX	NCBI_TaxID=7227;	
RN	[1]	
RP	SEQUENCE FROM N.A.	

RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Paclele J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.

RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Pargas V., Park S.,
RA Patel S., Phouaenavong S., Wan K., Yu C., Lewis S.E., Rudin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY060978; AAL28526.1; -.
DR EMBL: AY070894; AAL48516.1; -.
DR FlyBase: FBgn0003360; seeb.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carri_3.
DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_3.
SQ SEQUENCE 299 AA; 32909 MW; D51F3E2A70BD59E8 CRC64;

Query Match	81.0%	Score 1253.5	DB 5	Length 299
Best Local Similarity	81.2%	Pred. No. 6.9e-103		
Matches 237, Conservative	21	Mismatches 33	Indels 1	Gaps 1

Oy	5	ALSPKDELAGVAAASIKSTVAPPIERKLLLOVHASKOTTAPKQKGIIDCVIRPK	64
Oy	1		
Db	7	AVGFPKDPAAGISANASKTVAPIERKLLLOVHASKOTTAPKQKGIIDCVIRPK	66
Oy	65	QEVLSFMWGNLANVIRFEPYALNFAEKDKKYQIFLGVDKRRQFMWYFAGNLSAGGAG	124
Db	67	QGFSEFMWGNLANVIRFEPYALNFAEKDKKYQIFLGVDKRRQFMWYFAGNLSAGGAG	126
Oy	125	ATSLCFVYPLDFAFTRILADVQKGAEEFEGIDCIVKIKSGICIGLVGFVNSVQI	184
Db	127	ATSLCFVYPLDFAFTRILADVQK-GGQKEFEGIDCIVKIKSGICIGLVGFVNSVQI	185
Oy	185	IYRAAYGVIDTAKGMLPDRKNTIIVSNWIAOTVTVAVAGLTSYPPDYTRRRMMQSGR	244
Db	186	IYRAAYGVIDTAKGMLPDRKNTIIVSNWIAOTVTVAVAGLTSYPPDYTRRRMMQSGR	245
Oy	245	KGTDMITGTLDDCKRIARDEGCAAFKFGKANSNVLRCMGCAFVLYLDEIK	296
Db	246	KATEIYVNTNLHCWATJIAKOGTCAFFEGAFSNLIRGTGGAFVLYLDEIK	297

```

RESULT 11
09NHWS PRELIMINARY; PRT; 300 AA.
AC 09NHWS;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE ADP/ATP translocase
OS Lucilla cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidea; Calliphoridae; Lucilla.
OX NCBI_TaxID=7375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SS MAL SEEKING;
RA Chen Z., Fair J.A., Batterham P.;
RT "A CDNA clone encoding the ADP/ATP translocase of Lucilla cuprina." ;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF218587; AAF32322.1; -.
DR Interpro: IPR001993; Mitoch_carrier.

```


RESULT 14
 025129 PRELIMINARY: PRT: 304 AA.
 AC 025129;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE ADP/ATP translocase.
 GN HRA7L1.
 OS Halocynthia roretzi (Sea squirt).
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Pyuridae; Halocynthia.
 OX NCBI_TaxID=7729;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Miya T.;
 RL Submitted (Jan-1996) to the EMBL/GenBank/DBJ databases.
 RP [2]
 RP SEQUENCE FROM N.A.
 RA Miya T.;
 RL "Expression of a gene for major mitochondrial protein, ADP/ATP translocase, during embryogenesis in the ascidian Halocynthia roretzi."
 RT translocase, during embryogenesis in the ascidian Halocynthia roretzi."
 RL Dev. Growth Differ. 36:39-48(1994).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; D83069; BA01765.1; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carri. 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER. 3.
 DR Inner membrane; Mitochondrion; Transmembrane; Transport.
 KW SEQUENCE 304 AA; 33307 MW; 51FDD07D6B654880 CRC64;
 SQ
 Query Match 74.0%; Score 1145.5; DB 5; Length 304;
 Best Local Similarity 75.4%; Pred. No. 2.6e-93;
 Matches 221; Conservative 21; Mismatches 50; Indels 1; Gaps 1;
 Oy 4 AALSAKFLAGVAIAISKTAADIERVKLLQVQHASQITADKQYKGIIDCVVRIPK 63
 Db 4 SAVDEAKLAIIGGTAAAIKSTIVAPIERVKLLQVAVSTQKAGTEYKGIIDAFVRIPK 63
 Oy 64 EOEVSFPRGNLANIYRFPQALNFAFKDKKQIFLGVDKRTQFWRFAFNLASGGA 123
 Db 64 EGGFSLMRGNLANIYRFPQALNFAFKDKKQIFLGVDKRTQFWRFAFNLASGGA 123
 Oy 124 GATSLCFVYPLDFARTRLAADYGKAGAEERFGLDCLVKIKYSGIKGLYGFNVSYOG 183
 Db 124 GATGCLCFVYPLDFARTRLAADYG-SGGSKQFTGLGNCCLATYIKKQDPKGLYGFNVSYOG 182
 Oy 184 IIVYRAVFGIYDTAKGMLPDKPKNTHIYSNMAIQTVAVAGLSYRPFDTVRRMMOSG 243
 Db 184 IIVYRAVFGIYDTAKGMLPDKPKNTHIYSNMAIQTVAVAGLSYRPFDTVRRMMOSG 242
 Oy 244 RKGTLIMVTGTLDCWRKRIARDEGKAFKFGANSNLKRGKGFVLYLDEIKK 296
 Db 244 RKKEDRMVKGTVDCKWIKYKNGKAFKFGALSNVIRGTGALVLYLDELKK 295
 RESULT 15
 062526 PRELIMINARY: PRT: 307 AA.
 AC 062526;
 DT 01-AUG-1998 (TREMblrel. 07, Created)
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ANT2 protein.
 GN ANT2 OR CG1683.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Chapple M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.C.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekurov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paetle J.M.,
 RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Splier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtkas R., Tector C., Turner R., Venter L., Wang A., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenhach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-OREGON-R;
 RA Zhang Y.Q., Davis A.W., Roote J., Ashburner M.;
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003484; AAF47956.1; -
 DR EMBL; Y10618; CAH71629.1; -
 DR Flybase: FBgn0025111; Ant2.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carri. 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER. UNKNOWN 2.
 SQ SEQUENCE 307 AA; 33744 MW; 3D6B3D5FD8261C0C CRC64;
 Query Match 72.8%; Score 1125.5; DB 5; Length 307;
 Best Local Similarity 73.9%; Pred. No. 1.5e-91;
 Matches 215; Conservative 27; Mismatches 46; Indels 1; Gaps 1;
 Oy 7 SFAKDFLAGVAIAISKTAADIERVKLLQVQHASQITADKQYKGIIDCVVRIPK 66
 Db 17 SFLMPFMGVAIAIAKTAATVAPIERVKLLQVQHASQITADKQYKGIIDCVVRIPK 76
 Oy 67 VLSFMRGNLANIYRFPQALNFAFKDKKQIFLGVDKRTQFWRFAFNLASGGAAGT 126
 Db 77 ESSFMRGNLANIYRFPQALNFAFKDKKQIFLGVDKRTQFWRFAFNLASGGAAGT 136
 Oy 127 SLCFVYPLDFARTRLAADYGKAGAEERFGLDCLVKIKYSGIKGLYGFNVSYOGIIT 186
 Db 127 SLCFVYPLDFARTRLAADYGKAGAEERFGLDCLVKIKYSGIKGLYGFNVSYOGIIT 186

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:42:45 ; Search time 30.0336 Seconds
(without alignments)
1322.142 Million cell updates/sec

Title: US-09-393-441-33

Perfect score: 1543
Sequence: 1 MTEQAIISFADFLAGGIAA.....LRGCGAFVLVLDELKVI 298

Scoring table: BLOSUM62

Gap 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database :

1: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.*
2: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
3: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
4: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
5: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*
6: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.*
7: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.*
8: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.*
9: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.*
10: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.*
11: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.*
12: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
13: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.*
14: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.*
15: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT.*
16: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.*
17: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT.*
18: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.*
19: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
20: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	21	AAV71033 Human adenine nucl
2	1543	100.0	298	22	AAAM39641 Human polypeptide
3	1543	100.0	298	22	AAU01200 Human adenine nucl
4	1543	100.0	298	23	AAU10380 Human adenine nucl
5	1543	100.0	323	22	AAU41427 Human polypeptide
6	1454	94.2	298	21	AAV71032 Human adenine nucl
7	1454	94.2	298	22	AAU01199 Human adenine nucl
8	1454	94.2	298	23	AAU10379 Human adenine nucl
9	1412	91.5	298	19	AAAM6169 Anti protein. Mus
10	1385.5	89.8	297	21	AAV71031 Human adenine nucl

11	1385.5	89.8	297	22	AAU01198	Human adenine nucl
12	1385.5	89.8	297	23	AAU10378	Human adenine nucl
13	1367.5	88.6	325	22	ABG15422	Novel human diagno
14	1288	83.5	263	22	ABG27056	Novel human diagno
15	1254.5	81.3	299	22	ABM66082	Drosophila melanog
16	1254.5	81.3	299	22	ABM67300	Drosophila melanog
17	1137.5	73.7	307	22	ABM58380	Drosophila melanog
18	1119	72.5	315	22	AAE21175	Human TRICH-19 pro
19	1044	67.7	228	23	ABP43205	Human ovarian anti
20	879.5	57.0	298	22	ABG18922	Novel human diagno
21	763	49.4	484	22	ABG15422	Novel human diagno
22	763	49.4	484	22	ABG27055	Novel human diagno
23	749.5	48.6	386	22	AAU00106	ADP/ATP carrier pr
24	742.5	48.1	346	21	AAAG36577	Arabidopsis thalia
25	742.5	48.1	346	21	AAAG37261	Arabidopsis thalia
26	742.5	48.1	346	21	AAAG37264	Arabidopsis thalia
27	742.5	48.1	346	21	AAAG38460	Arabidopsis thalia
28	742.5	48.1	363	21	AAAG36576	Arabidopsis thalia
29	742.5	48.1	363	21	AAAG37260	Arabidopsis thalia
30	742.5	48.1	363	21	AAAG37263	Arabidopsis thalia
31	742.5	48.1	363	21	AAAG38459	Arabidopsis thalia
32	742.5	48.1	381	21	AAAG36575	Arabidopsis thalia
33	742.5	48.1	381	21	AAAG37259	Arabidopsis thalia
34	742.5	48.1	381	21	AAAG37262	Arabidopsis thalia
35	742.5	48.1	381	21	AAAG38458	Arabidopsis thalia
36	742.5	48.1	992	21	AAAG38672	Arabidopsis thalia
37	742.5	48.1	1009	21	AAAG38671	Arabidopsis thalia
38	742.5	48.1	1027	21	AAAG38670	Arabidopsis thalia
39	739.5	47.9	346	21	AAAG17731	Arabidopsis thalia
40	739.5	47.9	363	21	AAAG17730	Arabidopsis thalia
41	739.5	47.9	381	21	AAAG17729	Arabidopsis thalia
42	688.5	44.7	330	21	AAAG20658	Arabidopsis thalia
43	688.5	44.6	330	21	AAAG38398	Arabidopsis thalia
44	679.5	44.0	333	21	AAAG0857	Arabidopsis thalia
45	679.5	44.0	350	21	AAAG0856	Arabidopsis thalia

ALIGNMENTS

RESULT 1	AAV71033 standard; Protein: 298 AA.
ID	AAV71033
AC	AAV71033;
DT	29-AUG-2000 (first entry)
DE	Human adenine nucleotide translocator ANM3.
XX	Human: adenine nucleotide translocator; ANM3; mitochondria; ADP; ATP;
KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW	mitochondrial permeability translocator; neuroprotective; neurotrophic;
KW	antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW	antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW	diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIDU;
KW	mitochondrial diabetes and deafness; hyperproliferative disorder;
KW	myoclonic epilepsy red ragged fibre syndrome.
OS	Homo sapiens.
XX	WO200026370-A2.
PN	11-MAY-2000.
PD	03-NOV-1999; 99WO-US25863.
XX	03-NOV-1999; 99WO-US25863.
PF	03-NOV-1998; 98US-0185904.
PR	08-SEP-1998; 99US-0393441.
XX	(MITO-) MITOKOR.
PA	

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 XX
 DR WPI: 2000-365619/31.
 DR N-PSDB: AAD00521.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Claim 46: Page 173-174; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MID), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT3 from human brain.
 CC
 XX
 SQ Sequence 298 AA;

Query Match 100.0%; Score 1543; DB 21; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4,8e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQAISFADFLAGGIAAISTKTAIVAPIERVKLLQVHASKOIAADKOYKGIIVDCIVR 60
 DB 1 MTEQAISFADFLAGGIAAISTKTAIVAPIERVKLLQVHASKOIAADKOYKGIIVDCIVR 60
 QY 61 IPKQGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHNQFWRFFAGNLASG 120
 DB 61 IPKQGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHNQFWRFFAGNLASG 120
 QY 121 GAAGATSLCFYPPDLFARTRLAADVGKSGTERFERGLDCLVTKTSDGIRGLYOGFSYS 180
 DB 121 GAAGATSLCFYPPDLFARTRLAADVGKSGTERFERGLDCLVTKTSDGIRGLYOGFSYS 180
 QY 181 VOGIITIRAAVFGVYDTAKGMLPDPKNTHTLVSMIAQTVAAGVVSYPEDTVRRRMM 240
 DB 181 VOGIITIRAAVFGVYDTAKGMLPDPKNTHTLVSMIAQTVAAGVVSYPEDTVRRRMM 240
 QY 241 QSGRRKADIMYTGTCWRKIFRDEGGAFFKAGMSNVLRMGAFVLYLVDELKKVI 298
 DB 241 QSGRRKADIMYTGTCWRKIFRDEGGAFFKAGMSNVLRMGAFVLYLVDELKKVI 298

RESULT 2

AAM39641
 ID AAM39641 standard; Protein; 298 AA.

XX
 AC AAM39641;

XX
 DT 22-OCT-2001 (first entry)

XX
 DE Human polypeptide SEQ ID NO 2786.

XX Human; noctropic; immunosuppressant; cytosolic; gene therapy; cancer;
 KM peripheral nervous system; neuropathy; central nervous system; CNS;
 KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KM chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KM Leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000MO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 DR N-PSDB: AAI58797.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 PS Example 4; SEQ ID NO 2786; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with noctropic,
 CC immunosuppressant and cytosolic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX
 SQ Sequence 298 AA;
 Query Match 100.0%; Score 1543; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4,8e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQAISFADFLAGGIAAISTKTAIVAPIERVKLLQVHASKOIAADKOYKGIIVDCIVR 60
 DB 1 MTEQAISFADFLAGGIAAISTKTAIVAPIERVKLLQVHASKOIAADKOYKGIIVDCIVR 60
 QY 61 IPKQGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHNQFWRFFAGNLASG 120
 DB 61 IPKQGVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHNQFWRFFAGNLASG 120
 QY 121 GAAGATSLCFYPPDLFARTRLAADVGKSGTERFERGLDCLVTKTSDGIRGLYOGFSYS 180
 DB 121 GAAGATSLCFYPPDLFARTRLAADVGKSGTERFERGLDCLVTKTSDGIRGLYOGFSYS 180
 QY 181 VOGIITIRAAVFGVYDTAKGMLPDPKNTHTLVSMIAQTVAAGVVSYPEDTVRRRMM 240
 DB 181 VOGIITIRAAVFGVYDTAKGMLPDPKNTHTLVSMIAQTVAAGVVSYPEDTVRRRMM 240
 QY 241 QSGRRKADIMYTGTCWRKIFRDEGGAFFKAGMSNVLRMGAFVLYLVDELKKVI 298

DB 241 OSGRKGADIMYGTVDCKRKIFRDEGKAFFKGAMSNVLRGGAFFVLVYDELKKVI 298
 |||
 RESULT 3
 AAU01200
 ID AAU01200 standard; Protein: 298 AA.
 XX
 AC AAU01200;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human adenine nucleotide translocator-3 (ANT-3) protein.
 XX
 KM Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;
 KM mitochondrial permeability transition pore component; cell survival;
 KM mitochondrial core component; mitochondrial related disorder; cancer;
 KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PE 03-NOV-2000; 2000WO-US30535.
 XX
 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
 PI Vellicelebl G, Davis RE;
 DR MPI: 2001-291054/30.
 DR N-PSDB; AAS05903.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure: Fig 2; 186pp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-3
 CC (ANT-3) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 SQ Sequence 298 AA:
 Query Match 100.0%; Score 1543; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4,8e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MTEQAISFAKDFLACGIAAISKTAVAPIERVKLLQVOHASKQIAADKQYKGIQDCIVR 60
 DB 1 MTEQAISFAKDFLACGIAAISKTAVAPIERVKLLQVOHASKQIAADKQYKGIQDCIVR 60

OY 61 IPKEGCVLSFWRGNLAAVIRPEPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 |||
 DB 61 IPKEGCVLSFWRGNLAAVIRPEPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120
 OY 121 GAAGATSLCFVYPLDPARTRLAADYKSGSTEEFRLGDLCKYKRSQIRLKYGFSSVS 180
 |||
 DB 121 GAAGATSLCFVYPLDPARTRLAADYKSGSTEEFRLGDLCKYKRSQIRLKYGFSSVS 180
 OY 181 VGGIIYRAAYFGVYDTAKGMLPDPKNTIIYVSMIAQTVTAAGVSYPEPTVRRMM 240
 |||
 DB 181 VGGIIYRAAYFGVYDTAKGMLPDPKNTIIYVSMIAQTVTAAGVSYPEPTVRRMM 240
 OY 241 OSGRKGADIMYGTVDCKRKIFRDEGKAFFKGAMSNVLRGGAFFVLVYDELKKVI 298
 |||
 DB 241 OSGRKGADIMYGTVDCKRKIFRDEGKAFFKGAMSNVLRGGAFFVLVYDELKKVI 298
 RESULT 4
 AAU10380
 ID AAU10380 standard; Protein: 298 AA.
 XX
 AC AAU10380;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human adenine nucleotide translocator 3 (ANT3).
 XX
 KM Human; adenine nucleotide translocator; ANT;
 KM mitochondrial matrix protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200185944-A2.
 XX
 PD 15-NOV-2001.
 XX
 PE 11-MAY-2001; 2001WO-US15416.
 XX
 PR 11-MAY-2000; 2000US-0569327.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS, Moos WH, Pel Y, Carroll AK;
 DR MPI: 2002-055598/07.
 DR N-PSDB; AAS16690.
 XX
 PT Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide -
 XX
 PS Example 3: Fig 2; 147pp; English.
 XX
 CC The invention relates to a recombinant expression construct (1)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (1) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (1) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide, ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT3.

SQ Sequence 298 AA;

Query Match 100.0%; Score 1543; DB 23; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4,8e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQALSFANFDLAGGIAAIAISKTAVAPIERVKLLQVHASKQIAADKQKGIIVDCIVR 60
 1 MTEQALSFADFLAGGIAAIAISKTAVAPIERVKLLQVHASKQIAADKQKGIIVDCIVR 60
 DB 61 IPKQGVLSFWRGKLANVIRFPFOALNFAFKDKYKQIFLGVDKHKQFRRYFAGNLASG 120
 61 IPKQGVLSFWRGKLANVIRFPFOALNFAFKDKYKQIFLGVDKHKQFRRYFAGNLASG 120
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFGDGLVITKSDGRGLYQGSFVS 180
 121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFGDGLVITKSDGRGLYQGSFVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFGDGLVITKSDGRGLYQGSFVS 180
 121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFGDGLVITKSDGRGLYQGSFVS 180
 QY 181 VQGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSWMIAQVTAAGVSYFPDVTVRRMM 240
 181 VQGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSWMIAQVTAAGVSYFPDVTVRRMM 240
 DB 181 VQGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSWMIAQVTAAGVSYFPDVTVRRMM 240
 181 VQGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSWMIAQVTAAGVSYFPDVTVRRMM 240
 QY 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFKFGAMSIVLKGMGAFVLYLYDELKVI 298
 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFKFGAMSIVLKGMGAFVLYLYDELKVI 298
 DB 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFKFGAMSIVLKGMGAFVLYLYDELKVI 298

RESULT 5
 AAM41427
 ID AAM41427 standard; Protein; 323 AA.
 AC AAM41427;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 6358.
 XX
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemoketic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.
 KW
 XX Homo sapiens.
 OS
 XX
 PN WO200153312-A1.
 PD 26-JUL-2001.
 XX
 XX 26-DEC-2000; 2000MO-US34263.
 PF
 XX 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI; 2001-442253/47.
 DR N-PSDB; AAI60583.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX

PS Example 2; SEQ ID NO 6358; 10078bp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: immune system suppression, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed specification.
 CC
 SQ Sequence 323 AA;

Query Match 100.0%; Score 1543; DB 22; Length 323;
 Best Local Similarity 100.0%; Pred. No. 5,4e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQALSFANFDLAGGIAAIAISKTAVAPIERVKLLQVHASKQIAADKQKGIIVDCIVR 60
 26 MTEQALSFANFDLAGGIAAIAISKTAVAPIERVKLLQVHASKQIAADKQKGIIVDCIVR 85
 DB 61 IPKQGVLSFWRGKLANVIRFPFOALNFAFKDKYKQIFLGVDKHKQFRRYFAGNLASG 120
 86 IPKQGVLSFWRGKLANVIRFPFOALNFAFKDKYKQIFLGVDKHKQFRRYFAGNLASG 145
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFGDGLVITKSDGRGLYQGSFVS 180
 146 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFGDGLVITKSDGRGLYQGSFVS 205
 DB 181 VQGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSWMIAQVTAAGVSYFPDVTVRRMM 240
 206 VQGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSWMIAQVTAAGVSYFPDVTVRRMM 265
 DB 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFKFGAMSIVLKGMGAFVLYLYDELKVI 298
 266 QSGRKGADIMYTGTVDCWRKIFRDEGKAFKFGAMSIVLKGMGAFVLYLYDELKVI 323

RESULT 6
 AAY71032
 ID AAY71032 standard; Protein; 298 AA.
 AC AAY71032;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Human adenine nucleotide translocator ANT2.
 XX
 KW Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nootropic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.
 KW
 XX Homo sapiens.
 OS
 XX
 PN WO200026370-A2.
 PD 11-MAY-2000.
 XX

PF 03-NOV-1999; 99MO-US25883.
XX
PR 03-NOV-1999; 98US-0185904.
PR 08-SEP-1999; 99US-0393441.
XX
PA (MITO-) MITOKOR.
XX
PI Anderson CM, Davis RE, Clevenger W, Willey SE, Miller SM, Szabo TR;
PI Ghosh SS;
DR WPI; 2000-365619/31.
DR N-PSDB; AAD00520.
XX
PT Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease
XX
PS Claim 45; Page 172-173; 175pp; English.
XX
CC The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's disease, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MID), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT2 from human brain.
XX
SQ Sequence 298 AA:
Query Match 94.2%; Score 1454; DB 21; Length 298;
Best local Similarity 92.6%; Pred. No. 1.7e-147;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 1 MTEQATSFANDFLAGIAAISKTAAPIERVKLLQOVHASKQIADKQYKGIIVDCIVR 60
DB 1 MTEQATSFANDFLAGIAAISKTAAPIERVKLLQOVHASKQIADKQYKGIIVDCIVR 60
QY 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
DB 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVGKSTEREFRGLGDCLVKITSKGILYQGSFVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADVGKSTEREFRGLGDCLVKITSKGILYQGSFVS 180
QY 121 GAAGATSLCFVYPLDFARTRLADVGKSTEREFRGLGDCLVKITSKGILYQGSFVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADVGKSTEREFRGLGDCLVKITSKGILYQGSFVS 180
QY 181 VQGIITIRAAVFGVYDTAKMLPDPKNTHTIVSMIAQTVAAGVSYPTDVRRRMM 240
DB 181 VQGIITIRAAVFGVYDTAKMLPDPKNTHTIVSMIAQTVAAGVSYPTDVRRRMM 240
QY 241 QSGRKAGDIIYTGCTVDCWRKIFRDEGKAFKAGMSNVLRGKMGAFVLVYDELKK 296
DB 241 QSGRKAGDIIYTGCTVDCWRKIFRDEGKAFKAGMSNVLRGKMGAFVLVYDELKK 296
RESULT 7
AAU01199
ID AAU01199 standard; Protein; 298 AA.
XX
AC AAU01199;
XX
DT 07-SEP-2001 (first entry)
XX
DE Human adenine nucleotide translocator-2 (ANT-2) protein.

XX
KM Human: adenine nucleotide translocator-2; ANT-2; MPT; cyclophilin;
KM mitochondrial permeability transition pore component; cell survival;
KM mitochondrial core component; mitochondrial related disorder; cancer;
KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
XX
OS Homo sapiens.
PN WO200132876-A2.
XX
PD 10-MAY-2001.
XX
PF 03-NOV-2000; 2000MO-US30535.
XX
PR 03-NOV-1999; 99US-0434354.
XX
PA (MITO-) MITOKOR.
XX
PI Murphy AN, Clevenger W, Willey SE, Andreyev AY, Frliger LG;
PI Vellelebi G, Davis RE;
DR WPI; 2001-291054/30.
DR N-PSDB; AAS05902.
XX
PT New nucleic acid expression constructs, useful for screening for agents
PT that alter mitochondrial permeability transition (MPT), comprises
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
PT fused to energy transfer molecule -
XX
PS Disclosure; Fig 2; 166pp; English.
XX
CC The present sequence represents human adenine nucleotide translocator-2
CC (ANT-2) protein. ANT proteins are mitochondrial permeability
CC transition (MPT) pore components responsible for mediating transport
CC of ADP across the mitochondrial inner membrane. ANT proteins interact
CC with other mitochondrial core components e.g. cyclophilins to
CC regulate MPT. The present invention relates to a novel nucleic acid
CC expression construct comprising a promoter operably linked to a
CC polynucleotide encoding a mitochondrial pore component polypeptide
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
CC expression construct can alter mitochondrial membrane permeability
CC transition and/or alter the interaction between mitochondrial core
CC components. The methods are useful for screening for agents that alter
CC MPT and/or cell survival. These agents are useful for the prevention or
CC treatment of diseases associated with altered mitochondrial function or
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC mitochondrial encephalopathy, lactic acidosis, stroke, and deafness.
XX
SQ Sequence 298 AA:
Query Match 94.2%; Score 1454; DB 22; Length 298;
Best local Similarity 92.6%; Pred. No. 1.7e-147;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 1 MTEQATSFANDFLAGIAAISKTAAPIERVKLLQOVHASKQIADKQYKGIIVDCIVR 60
DB 1 MTEQATSFANDFLAGIAAISKTAAPIERVKLLQOVHASKQIADKQYKGIIVDCIVR 60
QY 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
DB 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVGKSTEREFRGLGDCLVKITSKGILYQGSFVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADVGKSTEREFRGLGDCLVKITSKGILYQGSFVS 180
QY 121 GAAGATSLCFVYPLDFARTRLADVGKSTEREFRGLGDCLVKITSKGILYQGSFVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADVGKSTEREFRGLGDCLVKITSKGILYQGSFVS 180
QY 181 VQGIITIRAAVFGVYDTAKMLPDPKNTHTIVSMIAQTVAAGVSYPTDVRRRMM 240
DB 181 VQGIITIRAAVFGVYDTAKMLPDPKNTHTIVSMIAQTVAAGVSYPTDVRRRMM 240

OY 241 QSGRKGADIMYTGIVDCWRKIFRDEGCKAFKFGKAMSNVLRMGCAFVLYLXDELK 296
 DB 241 QSGRKGADIMYTGIVDCWRKIFRDEGCKAFKFGKAMSNVLRMGCAFVLYLXDELK 296

RESULT 8

ID AAO10379 standard; Protein: 298 AA.

AAO10379;

14-FEB-2002 (first entry)

Human adenine nucleotide translocator 2 (ANT2).

Human: adenine nucleotide translocator; ANT; ss;

mitochondrial matrix protein.

Homo sapiens.

MO200185944-A2.

15-NOV-2001.

11-MAY-2001; 2001WO-US15416.

11-MAY-2000; 2000US-0569327.

(MITO-) MITOKOR.

Anderson CM, Davis RE, Cleverger W, Wiley SE, Miller SW, Szabo TR;

Ghosh SS, Moos WH, Pei Y, Carroll AK;

WPI: 2002-055598/07.

N-PSDB; AAS16689.

Novel recombinant expression construct for producing adenine nucleotide

translocator polypeptides, comprises a regulated promoter linked to

nucleic acid encoding the polypeptide

Claim 44; Fig 2; 147pp; English.

The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest. Recombinant ANT polypeptide, or cells expressing the polypeptide, is useful for identifying an agent that binds to an ANT polypeptide, ANT ligand is useful for determining the presence of an ANT polypeptide, preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating ANT from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANT2.

Sequence 298 AA:

Query Match 94.2%; Score 1454; DB 23; Length 298;

Best Local Similarity 92.6%; Pred. No. 1.7e-147;

Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

OY 1 MTEQAIISFAKDDLAGGIAAISKTAAPERKLLLOVHASKQIAADKQYGYDCTYR 60

DB 1 MTDALISFAKDDLAGGIAAISKTAAPERKLLLOVHASKQIAADKQYGYDCTYR 60

OY 61 IPKEGVLSFWFGNLANVRYPTQALNFAFKDKYKQIFLGVGVHDTQWRFFAGNLASG 120

DB 61 IPKEGVLSFWFGNLANVRYPTQALNFAFKDKYKQIFLGVGVHDTQWRFFAGNLASG 120

OY 121 GAAGATSLCFYVPLDFAETRLAADVGKSTEREERGLDCLVKITKSDGIRGLYQGFVS 180
 DB 121 GAAGATSLCFYVPLDFAETRLAADVGKSTEREERGLDCLVKITKSDGIRGLYQGFVS 180

OY 181 VQGIITRYAAAFGVYDTRAKGMLPPKKNHIVSWMIQOTVAVAGVSYSPEDTVRRMM 240

DB 181 VQGIITRYAAAFGVYDTRAKGMLPPKKNHIVSWMIQOTVAVAGVSYSPEDTVRRMM 240

OY 241 QSGRKGADIMYTGIVDCWRKIFRDEGCKAFKFGKAMSNVLRMGCAFVLYLXDELK 296

DB 241 QSGRKGADIMYTGIVDCWRKIFRDEGCKAFKFGKAMSNVLRMGCAFVLYLXDELK 296

RESULT 9

ID AAW61169 standard; Protein: 298 AA.

AAW61169;

28-SEP-1998 (first entry)

Ant1 protein.

Ant1; Adenine nucleotide translocator; cloning; screening;

DNA Tag diodeoxy terminator cycle sequencing; oxidative phosphorylation;

probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;

hypertrophic cardiomyopathy; fasciocalcular humeral muscular dystrophy;

lactic acidosis; degenerative muscle disease.

Mus sp.

WO9819714-A1.

14-MAY-1998.

31-OCT-1997; 97WO-US19882.

01-NOV-1996; 96US-0030017.

(UYEM-) UNIV EMORY.

Graham BC, Macgregor GR, Wallace DC;

WPI: 1998-286608/25.

N-PSDB; AAV36479.

Mice lacking heart-muscle adenine nucleotide translocator protein -

useful as model for mitochondrial myopathy and hypertrophic

cardiomyopathy in animals and to test therapeutic compositions or

gene therapies

Disclosure: Page 39-40; 61pp; English.

The present sequence is the mouse Ant1 protein, the cDNA producing this polypeptide is cloned by screening a mouse heart cDNA library with the human Ant1 cDNA as a probe. The Ant1 cDNA sequence was determined by DNA Tag diodeoxy terminator cycle sequencing. The Ant1 protein is encoded by the Ant1 locus, a nuclear gene on chromosome 8. This protein is required in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which can then be converted into ATP. An Ant1 homozygous mutant would thus be defective in OXPHOS which results in disease in oxidative metabolism dependent tissues. This mouse Ant1 homozygous mutant can be used as a model system for fasciocalcular humeral muscular dystrophy, hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model systems can be used to test possible therapeutic compounds which increase/mediate ATP and ADP exchange across the mitochondrial membrane independent of Ant1.

Sequence 298 AA:

Query Match 91.5%; Score 1412; DB 19; Length 298;

Best Local Similarity 88.6%; Pred. No. 5.6e-143;

XX Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR N-PSDB; AAS79610.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID No 45782; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 XX
 SQ Sequence 325 AA;
 Query Match 88.6%; Score 1367.5; DB 22; Length 325;
 Best Local Similarity 88.0%; Pred. No. 3.8e-138;
 Matches 263; Conservative 13; Mismatches 20; Indels 3; Gaps 2;
 QY 1 MTEQAISFAKDFTAGTAAIAISKTAVAPIERVKLLQVHASKQIADKQYKGIIVDCIVR 60
 DB 24 MTEAASVAFADFLAGVAAIAISKTAVAPIERVKLLQVHASKQIADKQYKGIIVDCIVR 83
 QY 61 IPKEQGLSTFWRGKLANVIRFPQALNFAFKDKYKQIFLGVDVKHOFMRFGAGNLASG 120
 DB 84 IPKEQGLSTFWRGKLANVIRFPQALNFAFKDKYKQIFLGVDVKHOFMRFGAGNLASG 143
 QY 121 GAAGATSLCEVYPLDFARTRLAADVGKSTEREFRLGDCIVKTKSDGINTLQGFSSVS 180
 DB 144 GAAGATSLCEVYPLDFARTRLAADVGKATEREFGDCLVKTKSDGINTLQGFSSVS 203
 QY 181 VGGIITRAAYFGYDTAKGMLPDPKTHIVSMIAQTV-TAAVAGVYSTPFDV--VRRR 237
 DB 204 VGGIITRAAYFGYDTAKGMLPDPKTHIVSMIAQTVHCCGCGXLPYFPFDRSVARN 263

QY 238 MMQSGRKGADIMYTGVDCKRIERDEGKAFFKGAWSVNLKMGSAFVLVYDELKK 296
 DB 264 EXMQSGRKGADIMYTGVDCKRIARDEGKAFFKGAWSVNLKMGSAFVLVYELKSK 322
 RESULT 14
 ID ABG27056
 ID ABG27056 standard; Protein; 263 AA.
 AC ABG27056;
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #27047.
 XX
 KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR N-PSDB; AAS91243.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID No 57415; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 XX
 SQ Sequence 263 AA;
 Query Match 83.5%; Score 1288; DB 22; Length 263;
 Best Local Similarity 92.7%; Pred. No. 9.6e-130;
 Matches 242; Conservative 12; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MTEQAISFAKDFTAGTAAIAISKTAVAPIERVKLLQVHASKQIADKQYKGIIVDCIVR 60
 DB 24 MTEAASVAFADFLAGVAAIAISKTAVAPIERVKLLQVHASKQIADKQYKGIIVDCIVR 83

Db 1 MTDAVSEAFKDFLAGGVAALISKTAVAPIERVKLLLOVQHASKQITPADKQYKGIIDCVVR 60
Qy 61 IPKEGVSLFPMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
Db 61 IPKEGVSLFPMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
Qy 121 GAAGATSLCFVYPLDFAFTRLAADYKSGTEREPRGLDCLVKIRKSDGIRGLYOGFSVS 180
Db 121 GAAGATSLCFVYPLDFAFTRLAADYKSGTEREPRGLDCLVKIRKSDGIRGLYOGFSVS 180
Qy 181 VOGIIYAAAFGVYDTRAKGMLPDPKNTHIYVSMIAQTVTAAGVSYPTVRRMM 240
Db 181 VOGIIYAAAFGVYDTRAKGMLPDPKNTHIYVSMIAQTVTAAGVSYPTVRRMM 240
Qy 241 QSGRKADIMYTGIVDCWKRI 261
Db 241 QSGRKGTDMYTGITDCWKRI 261

RESULT 15

ABB66082
ID ABB66082 standard; Protein; 299 AA.

AC ABB66082;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 25038.

KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI: 2001-656860/75.

DR N-PSDB; ABL10185.

PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -

PS Disclosure; SEQ ID NO 25038; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB16176-AB130511), expressed DNA sequences (AB101840-AB16175) and the encoded proteins (AB161737-AB162072).
CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 299 AA;

Qy 5 AISEFAKDFLAGGIAAALISKTAVAPIERVKLLLOVQHASKQIADKQYKGIIVDCIARIPE 64
Db 7 AVGFYKDFDAAGISAAVSKTAVAPIERVKLLLOVQHISKQISPDKQYKGMVDCFIIRPE 66
Qy 65 QGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASGGAAG 124
Db 67 QGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASGGAAG 126
Qy 125 ATSLCFVYPLDFAFTRLAADYKSGTEREPRGLDCLVKIRKSDGIRGLYOGFSVSOGI 184
Db 127 ATSLCFVYPLDFAFTRLAADYKSG-QREFTGLGMLTKIRKSDGIRGLYOGFSVSOGI 185
Qy 185 IIRAAVFGVYDTRAKGMLPDPKNTHIYVSMIAQTVTAAGVSYPTVRRMMMSG 244
Db 186 IIRAAVFGVYDTRAKGMLPDPKNTPIYVSMIAQVTTVAGIVSYPTVRRMMMSG 245
Qy 245 KGADIMYTGIVDCWKRIFRDEGKAFKFGANSNVLKMGCAFVLVYDELKKVI 298
Db 246 KATEVIVKNTLHCWATIAKOBEGTGAFFKGAFAFSNLTGCGAFVLVYDELKKVL 299

Search completed: November 12, 2002, 16:45:58
Job time : 31.0336 secs

Query Match 81.3%; Score 1254.5; DB 22; Length 299;
Best Local Similarity 80.6%; Pred. No. 4.5e-126;
Matches 237; Conservative 23; Mismatches 33; Indels 1; Gaps 1;

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:44:25 : Search time 11.6797 seconds
(without alignments)
750.705 million cell updates/sec

Title: US-09-393-441-33
Perfect score: 1543
Sequence: 1 MTEQAISFAKDFLAGIAA.....LRGMGAFLVLYDELKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued_Patents_AA:*
2: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/BACKLIST1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1412	91.5	298	3	US-08-961-871-10
2	311	20.2	469	4	US-09-188-930-339
3	283.5	18.4	291	4	US-09-501-558-2
4	280	18.1	447	4	US-09-160-119-2
5	280	18.1	674	4	US-09-160-119-2
6	265	17.2	312	4	US-09-142-565-2
7	250.5	16.2	299	1	US-08-518-878B-56
8	250.5	16.2	299	2	US-08-470-868A-56
9	250.5	16.2	309	1	US-08-518-878B-51
10	250.5	16.2	309	2	US-08-807-861A-51
11	250.5	16.2	309	3	US-08-470-868A-51
12	250.5	16.2	309	3	US-09-210-681-51
13	250.5	16.2	309	3	US-08-946-719A-51
14	250.5	16.2	311	2	US-08-937-466-4
15	245	15.9	432	2	US-08-937-466-4
16	245	15.9	432	2	US-09-172-528-4
17	245	15.9	432	2	US-09-118-199-4
18	245	15.9	432	4	US-09-503-579-4
19	244	15.8	308	2	US-08-937-466-2
20	244	15.8	308	2	US-09-172-528-2
21	244	15.8	308	3	US-09-318-199-2
22	244	15.8	308	4	US-09-503-579-2
23	243.5	15.8	311	2	US-08-775-009-32
24	232.5	15.1	320	2	US-08-933-750C-12
25	232.5	15.1	320	4	US-09-234-613-12
26	227.5	14.7	303	1	US-08-294-522B-36
27	226.5	14.7	303	1	US-08-518-878B-37

28	226.5	14.7	303	2	US-08-807-861A-37	Sequence 37, Appl
29	226.5	14.7	303	2	US-08-470-868A-37	Sequence 37, Appl
30	226.5	14.7	303	3	US-09-210-681-37	Sequence 37, Appl
31	226.5	14.7	303	3	US-08-946-719A-37	Sequence 37, Appl
32	222	14.4	293	4	US-09-501-558-4	Sequence 4, Appl1
33	222	14.4	306	5	PCT-US94-09799-1	Sequence 1, Appl1
34	205.5	13.3	307	2	US-08-807-861A-56	Sequence 56, Appl
35	205.5	13.3	307	3	US-09-210-681-56	Sequence 56, Appl
36	205.5	13.3	307	3	US-08-946-719A-56	Sequence 56, Appl
37	198.5	12.9	351	2	US-08-933-750C-19	Sequence 19, Appl
38	198.5	12.9	351	4	US-09-234-613-19	Sequence 19, Appl
39	193	12.5	328	4	US-09-068-140A-15	Sequence 15, Appl
40	191	12.4	256	2	US-08-937-466-6	Sequence 6, Appl1
41	191	12.4	256	2	US-09-172-528-6	Sequence 6, Appl1
42	191	12.4	256	3	US-09-318-199-6	Sequence 6, Appl1
43	191	12.4	256	4	US-09-503-579-6	Sequence 6, Appl1
44	181	11.7	289	4	US-09-068-140A-10	Sequence 10, Appl
45	180.5	11.7	312	4	US-09-188-930-142	Sequence 142, Appl

ALIGNMENTS

RESULT 1
US-08-961-871-10
: Sequence 10, Application US/08961871
: Patent No. 6013658
: GENERAL INFORMATION:
: APPLICANT: Wallace, Douglas C.
: APPLICANT: Graham, Brett H.
: APPLICANT: Macgregor, Grant R.
: TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
: TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
: STREET: 5370 Manhattan Circle, Suite 201
: City: Boulder
: STATE: Colorado
: COUNTRY: US
: ZIP: 80303
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/961,871
: FILING DATE: 31-OCT-1997
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/030,017
: FILING DATE: 01-NOV-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Ferber, Donna M.
: REGISTRATION NUMBER: 33,878
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (303) 499-8089
: TELEFAX: (303) 499-8089
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 298 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-961-871-10

Query Match 91.5%; Score 1412; DB 3; Length 298;
Best Local Similarity 88.6%; Pred. No. 2.2e-151;
Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;
QY 1 MTEQAISFAKDFLAGIAAISKRAVAPIRVKLLLVGHASKQIADKQKIVDCIVR 60

RESULT 3
US-09-501-558-2
; Sequence 2, Application US/09501558
; Patent No. 6403784
; GENERAL INFORMATION:

Query Match	18.13;	Score 280;	DB 4;	Length 447;
Best Local Similarity	27.13;	Pred. No. 3.9e-23;		
Matches 80; Conservative	47;	Mismatches 148;	Indels 20;	Gaps 6

RESULT 6
US-09-142-565-2

ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-518-878B-56

Query Match 16.2%; Score 250.5; DB 1; Length 299;
Best Local Similarity 24.9%; Pred. No. 4.7e-20;
Matches 74; Conservative 52; Mismatches 146; Indels 25; Gaps 8;

QY 12 FLAGGIAAISKTAVERPIERKLLQVQHASK--QIAADKQYKGIYDCIIRPEQGV 68
DB 7 FLAGGTAACIADLTFFLDFAKVRLOIGESQGPVRAVSAQYGVNGTILTVRTGPR 66
QY 69 SFMGNLANVIRYPTQALNFAFDKTKQIFLGVDKHTQWRIFAGNLASGGAAGTSL 128
DB 67 SLYNGLVAGLQROMSFASVIRGLYDSVKQFYTKG-SEHAS---IGSRLLAGSTTGALAV 121
QY 129 CFVYPLFAPTRLAADGKSGTEREPRGLDCLVKITKSDGIRGLYGFVSVOGIIYR 188
DB 122 AVAOPDVVKYRFOAQ-ARAGGRRYOSTVNAVYKTIAREGEFRGLMKTSPNVARNAIVN 180
QY 189 AAYFGVYDTAK-----GMLPDPKNTIHVSWMTAQVTAVAGVSYFPTVRRMMQOS 242
DB 181 CAELVTYDLIKDALLLKANLMTDPLCHFTSAFAGFCTVIAS---PVDVVKTRYM--- 233
QY 243 GRKADIMYGTVCWKIRFDEGKAFKFGAMSNVLR-GMGCAFVLYLDELKVI 298
DB 234 --NSALQOYSAGHCALTMLOKEGPRAFYKGFMPFLRLSGMNVNMYEYOLKRAL 288

RESULT 8
US-08-470-868A-56
Sequence 56, Application US/08470868A
Patent No. 5861485
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 299 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-470-868A-56

Query Match 16.2%; Score 250.5; DB 2; Length 299;
Best Local Similarity 24.9%; Pred. No. 4.7e-20;
Matches 74; Conservative 52; Mismatches 146; Indels 25; Gaps 8;

QY 12 FLAGGIAAISKTAVERPIERKLLQVQHASK--QIAADKQYKGIYDCIIRPEQGV 68
DB 7 FLAGGTAACIADLTFFLDFAKVRLOIGESQGPVRAVSAQYGVNGTILTVRTGPR 66
QY 69 SFMGNLANVIRYPTQALNFAFDKTKQIFLGVDKHTQWRIFAGNLASGGAAGTSL 128
DB 67 SLYNGLVAGLQROMSFASVIRGLYDSVKQFYTKG-SEHAS---IGSRLLAGSTTGALAV 121
QY 129 CFVYPLFAPTRLAADGKSGTEREPRGLDCLVKITKSDGIRGLYGFVSVOGIIYR 188
DB 122 AVAOPDVVKYRFOAQ-ARAGGRRYOSTVNAVYKTIAREGEFRGLMKTSPNVARNAIVN 180
QY 189 AAYFGVYDTAK-----GMLPDPKNTIHVSWMTAQVTAVAGVSYFPTVRRMMQOS 242
DB 181 CAELVTYDLIKDALLLKANLMTDPLCHFTSAFAGFCTVIAS---PVDVVKTRYM--- 233
QY 243 GRKADIMYGTVCWKIRFDEGKAFKFGAMSNVLR-GMGCAFVLYLDELKVI 298
DB 234 --NSALQOYSAGHCALTMLOKEGPRAFYKGFMPFLRLSGMNVNMYEYOLKRAL 288

RESULT 9
US-08-518-878B-51
Sequence 51, Application US/0851878B
Patent No. 5702902
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:

Query Match	16.28	Score	250.5	DB 2	Length	309
Best Local Similarity	24.98	Pred.	NO. 4.9e-20			
Matches	74	Conservative	52	Mismatches	146	Indels
					25	Gaps
						8
QY	12	FLAGIAAAISTKTVPADIERVKLLLOVHNSK---QIAADQKQKGLVDICVRIPKEGVL	68			
		: : : : : : : :				
Db	17	FLGAGTAACTADLTFFLPDPAKVAQLQGSQSGGVKRVATVSAQVRGVAIGTLLTWKREGPR	76			
QY	69	SEWRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNINLASGAAGATSL	128			
		: : : : : : : : :				
Db	77	SLYNGIVAGLGRQKSFASVRIGLVDYSKVQYTKG-SEHAS----ISRLLAGSTTGALAV	131			
QY	129	CFVVPDLPFAKRIAADVKSCTEREFFGLDCLVTKTSKSGINGLTOIGSFVSVOGIITIR	188			
		: : : : : : : : : : :				
Db	132	AVAAPTDVWKYRFQAO--ARAGGGRRYOSTVANAKYTTIAREEGFGLMKGTSPTNARAIYA	190			
QY	189	AAAFGVVDLAK-----GMLPDPKNTHTIVASMTAQVTVAVAGVSVSEFPTVRRRMMS	242			
		: : : : : : : : : :				
Db	191	CAELVTYDLKLDALLKANLMTVDLPCHTSAFGAGFCTTIVAS---PVDVVTTRYA---	243			
QY	243	GRKGADIIYTTGTVCWKRIFRDEGGKAFKFGAMSNYLR--GMGAFYLVLDLKKYI	298			
		: : : : : : : : : :				
Db	244	--NSALGYSAGCALTMLQKEGPRAFYVGFEMPSFLRLSSMNVMVETVEQLKRAL	298			

RESULT 12
US-09-210-681-51
Sequence 51, Application US/09210681
Patent No. 6057109
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cortuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown

Query Match	16.2%	Score 250.5	DB 3	Length 309
Best Local Similarity	24.9%	Pred. No. 4.9e-20		
Matches 74	Conservative 52	Mismatches 146	Indels 25	Gaps 8
Qy	12	FLAGLIAAIAISTAAVAPIERVKLLVOYHASK---	QIADRKQYKGIVDPIRPEQGVL	68
		:: :: :: :: :: :: :: ::	:: :: :: :: :: :: :: ::	
Dd	17	FLAGAGTAACIADLIFFPLDPTAKYRLQIGESGSPRAIYSAOIRGVMGITLIMVREGR		76
		:: :: :: :: :: :: :: ::	:: :: :: :: :: :: :: ::	
Qy	69	SFMRGNLANVIRYFPFTOLNFAFKDKYKQIFLGVDKHTQFWRYPAGNLIASGAAGATSL		128
		:: :: :: :: :: :: :: ::	:: :: :: :: :: :: :: ::	
Dd	77	SLYINGLVAGLQOMSPASVIRIGLYSVQFYTKG--SEHNS----	IGSRLLASTGTGALAAV	131
		:: :: :: :: :: :: :: ::	:: :: :: :: :: :: :: ::	
Qy	129	CFVYPLDPARTRFLAADVGKSGSTEREERGLGCDLVKITKSDGIRGLYOGFSVVOGIIYR		188
		:: :: :: :: :: :: :: ::	:: :: :: :: :: :: :: ::	
Dd	133	AVAQEPIDVVKVYRFQAO--ARACGGRRYQSTVNAKYTLIAREEGRGLMKGTSPVVARNAIYN		190
		:: :: :: :: :: :: :: ::	:: :: :: :: :: :: :: ::	
Qy	169	AAVPEGVYDPAK-----GMLPDPKNTHIYVSMMIAQTYAAVGVSYPPDYVRRRMQMS		242
		:: :: :: :: :: :: :: ::	:: :: :: :: :: :: :: ::	
Dd	191	CAELVYTYDILIKALLKANIMLTDDLPCHFTSAGAGFCTTIVAS---	PVDVVKTRYM---	243
		:: :: :: :: :: :: :: ::	:: :: :: :: :: :: :: ::	
Qy	243	GRRGADIWTTGTGVDCWRKIFRDEGKGAFKFGKAMSVULR--GMGCAVLYLYDELLKVI		298
		:: :: :: :: :: :: :: ::	:: :: :: :: :: :: :: ::	
Dd	244	--NSALGQYSSAGHCALITMLOKEGRATFKGIMPSPFLRLGSSNNVNMVFYIYEDLKRAL		298

```

1      RESULT 13
2      US-08-946-719A-51
3      ; Sequence 51, Application US/08946719A
4      ; Patent No. 6121017
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Tartaglia, Louis A.
7      ; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
8      ; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
9      ; NUMBER OF SEQUENCES: 64
10     ; CORRESPONDENCE ADDRESS:
11     ; ADDRESSEE: Pennie & Edmonds LLP
12     ; STREET: 1155 Avenue of the Americas
13     ; CITY: New York
14     ; STATE: New York
15     ; COUNTRY: U.S.A.
16     ; ZIP: 10036-2711
17     ; COMPUTER READABLE FORM:
18     ; MEDIUM TYPE: Floppy disk
19     ; COMPUTER: IBM PC Compatible
20     ; OPERATING SYSTEM: PC-DOS/MS-DOS
21     ; SOFTWARE: PatentIn Release #1.0, Version #1.30
22     ; CURRENT APPLICATION DATA:
23     ; APPLICATION NUMBER: US/08/946,719A
24     ; FILING DATE: 8-OCT-1997
25     ; CLASSIFICATION: 435
26     ; PRIOR APPLICATION DATA:
27     ; APPLICATION NUMBER: US 08/807,861
28     ; FILING DATE: 26-FEB-1997
29     ; APPLICATION NUMBER: US 08/518,878
30     ; FILING DATE: 23-AUG-1995
31     ; APPLICATION NUMBER: US 08/470,868
32     ; FILING DATE: 06-JUN-1995
33     ; APPLICATION NUMBER: US 08/294,522
34     ; FILING DATE: 23-AUG-1994
35     ; ATTORNEY/AGENT INFORMATION:
36     ; NAME: Coruzzi, Laura A.
37     ; REGISTRATION NUMBER: 30,742
38     ; TELECOMMUNICATION INFORMATION:
39     ; TELEPHONE: (212) 790-9090
40     ; TELEFAX: (212) 869-9741/8864
41     ; TELEX: 66141 PENNIE
42     ; INFORMATION FOR SEQ ID NO: 51:
43     ; SEQUENCE CHARACTERISTICS:
44     ; LENGTH: 309 amino acids
45     ; TYPE: amino acid
46     ;
47     ;
48     ;
49     ;
50     ;
51     ;
52     ;
53     ;
54     ;
55     ;
56     ;
57     ;
58     ;
59     ;
60     ;
61     ;
62     ;
63     ;
64     ;
65     ;
66     ;
67     ;
68     ;
69     ;
70     ;
71     ;
72     ;
73     ;
74     ;
75     ;
76     ;
77     ;
78     ;
79     ;
80     ;
81     ;
82     ;
83     ;
84     ;
85     ;
86     ;
87     ;
88     ;
89     ;
90     ;
91     ;
92     ;
93     ;
94     ;
95     ;
96     ;
97     ;
98     ;
99     ;
100    ;
101    ;
102    ;
103    ;
104    ;
105    ;
106    ;
107    ;
108    ;
109    ;
110    ;
111    ;
112    ;
113    ;
114    ;
115    ;
116    ;
117    ;
118    ;
119    ;
120    ;
121    ;
122    ;
123    ;
124    ;
125    ;
126    ;
127    ;
128    ;
129    ;
130    ;
131    ;
132    ;
133    ;
134    ;
135    ;
136    ;
137    ;
138    ;
139    ;
140    ;
141    ;
142    ;
143    ;
144    ;
145    ;
146    ;
147    ;
148    ;
149    ;
150    ;
151    ;
152    ;
153    ;
154    ;
155    ;
156    ;
157    ;
158    ;
159    ;
160    ;
161    ;
162    ;
163    ;
164    ;
165    ;
166    ;
167    ;
168    ;
169    ;
170    ;
171    ;
172    ;
173    ;
174    ;
175    ;
176    ;
177    ;
178    ;
179    ;
180    ;
181    ;
182    ;
183    ;
184    ;
185    ;
186    ;
187    ;
188    ;
189    ;
190    ;
191    ;
192    ;
193    ;
194    ;
195    ;
196    ;
197    ;
198    ;
199    ;
200    ;
201    ;
202    ;
203    ;
204    ;
205    ;
206    ;
207    ;
208    ;
209    ;
210    ;
211    ;
212    ;
213    ;
214    ;
215    ;
216    ;
217    ;
218    ;
219    ;
220    ;
221    ;
222    ;
223    ;
224    ;
225    ;
226    ;
227    ;
228    ;
229    ;
230    ;
231    ;
232    ;
233    ;
234    ;
235    ;
236    ;
237    ;
238    ;
239    ;
240    ;
241    ;
242    ;
243    ;
244    ;
245    ;
246    ;
247    ;
248    ;
249    ;
250    ;
251    ;
252    ;
253    ;
254    ;
255    ;
256    ;
257    ;
258    ;
259    ;
260    ;
261    ;
262    ;
263    ;
264    ;
265    ;
266    ;
267    ;
268    ;
269    ;
270    ;
271    ;
272    ;
273    ;
274    ;
275    ;
276    ;
277    ;
278    ;
279    ;
280    ;
281    ;
282    ;
283    ;
284    ;
285    ;
286    ;
287    ;
288    ;
289    ;
290    ;
291    ;
292    ;
293    ;
294    ;
295    ;
296    ;
297    ;
298    ;
299    ;
300    ;
301    ;
302    ;
303    ;
304    ;
305    ;
306    ;
307    ;
308    ;
309    ;
310    ;
311    ;
312    ;
313    ;
314    ;
315    ;
316    ;
317    ;
318    ;
319    ;
320    ;
321    ;
322    ;
323    ;
324    ;
325    ;
326    ;
327    ;
328    ;
329    ;
330    ;
331    ;
332    ;
333    ;
334    ;
335    ;
336    ;
337    ;
338    ;
339    ;
340    ;
341    ;
342    ;
343    ;
344    ;
345    ;
346    ;
347    ;
348    ;
349    ;
350    ;
351    ;
352    ;
353    ;
354    ;
355    ;
356    ;
357    ;
358    ;
359    ;
360    ;
361    ;
362    ;
363    ;
364    ;
365    ;
366    ;
367    ;
368    ;
369    ;
370    ;
371    ;
372    ;
373    ;
374    ;
375    ;
376    ;
377    ;
378    ;
379    ;
380    ;
381    ;
382    ;
383    ;
384    ;
385    ;
386    ;
387    ;
388    ;
389    ;
390    ;
391    ;
392    ;
393    ;
394    ;
395    ;
396    ;
397    ;
398    ;
399    ;
400    ;
401    ;
402    ;
403    ;
404    ;
405    ;
406    ;
407    ;
408    ;
409    ;
410    ;
411    ;
412    ;
413    ;
414    ;
415    ;
416    ;
417    ;
418    ;
419    ;
420    ;
421    ;
422    ;
423    ;
424    ;
425    ;
426    ;
427    ;
428    ;
429    ;
430    ;
431    ;
432    ;
433    ;
434    ;
435    ;
436    ;
437    ;
438    ;
439    ;
440    ;
441    ;
442    ;
443    ;
444    ;
445    ;
446    ;
447    ;
448    ;
449    ;
450    ;
451    ;
452    ;
453    ;
454    ;
455    ;
456    ;
457    ;
458    ;
459    ;
460    ;
461    ;
462    ;
463    ;
464    ;
465    ;
466    ;
467    ;
468    ;
469    ;
470    ;
471    ;
472    ;
473    ;
474    ;
475    ;
476    ;
477    ;
478    ;
479    ;
480    ;
481    ;
482    ;
483    ;
484    ;
485    ;
486    ;
487    ;
488    ;
489    ;
490    ;
491    ;
492    ;
493    ;
494    ;
495    ;
496    ;
497    ;
498    ;
499    ;
500    ;
501    ;
502    ;
503    ;
504    ;
505    ;
506    ;
507    ;
508    ;
509    ;
510    ;
511    ;
512    ;
513    ;
514    ;
515    ;
516    ;
517    ;
518    ;
519    ;
520    ;
521    ;
522    ;
523    ;
524    ;
525    ;
526    ;
527    ;
528    ;
529    ;
530    ;
531    ;
532    ;
533    ;
534    ;
535    ;
536    ;
537    ;
538    ;
539    ;
540    ;
541    ;
542    ;
543    ;
544    ;
545    ;
546    ;
547    ;
548    ;
549    ;
550    ;
551    ;
552    ;
553    ;
554    ;
555    ;
556    ;
557    ;
558    ;
559    ;
560    ;
561    ;
562    ;
563    ;
564    ;
565    ;
566    ;
567    ;
568    ;
569    ;
570    ;
571    ;
572    ;
573    ;
574    ;
575    ;
576    ;
577    ;
578    ;
579    ;
580    ;
581    ;
582    ;
583    ;
584    ;
585    ;
586    ;
587    ;
588    ;
589    ;
590    ;
591    ;
592    ;
593    ;
594    ;
595    ;
596    ;
597    ;
598    ;
599    ;
600    ;
601    ;
602    ;
603    ;
604    ;
605    ;
606    ;
607    ;
608    ;
609    ;
610    ;
611    ;
612    ;
613    ;
614    ;
615    ;
616    ;
617    ;
618    ;
619    ;
620    ;
621    ;
```



```
Db 17 FLAGGTACEFADLLTFPLDIAKVRLOIQ-GENPGAQSVQYRGVGLGTLITWVRETEGPRSPY 75
QY 72 RGNLANVIRYPPPTQALNPAFMDKVKQJFELGVDKHTQFMRYFAGNLAGGAAGATSLCFV 131
Db 76 SGLVAGLHRQMSFASIRIGLYDSVKQFYTPKGADHSS----VAIRILAGCTTGMAAVTCA 131
QY 132 YPLDFAARTRLAADVG-KSGTEREPRGLGDLVKITKSDGINGLYQGFSSVQGIITVRAA 190
Db 132 QPTDVVKKVRFQAMIRLGTGGERKRYGTMDAVRTIAREGVRGLWKGTWPNITRNAIVNCA 191
QY 191 YFGYDPAKGMLPDPKNTNHYVSMIAQVTA-----VAGVSYTPEDTVRRRAA-MQSGR 244
Db 192 EMVTYDIKEKLE---SHLETDNFPCHFVSAFGAGFCATVVASPDVVKTRYMNAPLGR 248
QY 245 KGADIMYTGTVDCWRKIIFRDEGKAFPKAGASNYLR--GMGGAFLVLYDELKVTI 298
Db 249 -----YRSPILCHMLKNVAOEGPTAFYKGFVPSFLRLGAMNMVFYIEQLKRAL 297
```

Search completed: November 12, 2002, 16:49:20
job time : 13.0131 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:47:56 : Search time 6.34043 Seconds
(Without alignments)
677.670 Million cell updates/sec

Title: US-09-393-441-33
Perfect score: 1543
Sequence: 1 MTEQAISPAKDFLAGGIAA.....LRMGAFVLVLDLKKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 92612 seqs, 14418503 residues

Total number of hits satisfying chosen parameters: 92612

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB pep:*
2: /cgn2_6/ptodata/1/pubppa/PCR_NEW_PUB pep:*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB pep:*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB pep:*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB pep:*
6: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB pep:*
7: /cgn2_6/ptodata/1/pubppa/PCUS_PUBCOMB pep:*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB pep:*
9: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB pep:*
10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB pep:*
11: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB pep:*
12: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB pep:*
13: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB pep:*
14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	10	US-09-811-094-33 Sequence 33, Appl
2	1543	100.0	298	10	US-09-810-644-33 Sequence 33, Appl
3	1454	94.2	298	10	US-09-811-094-32 Sequence 32, Appl
4	1454	94.2	298	10	US-09-810-644-32 Sequence 32, Appl
5	1385.5	89.8	297	10	US-09-811-094-31 Sequence 31, Appl
6	1385.5	89.8	297	10	US-09-810-644-31 Sequence 31, Appl
7	760.5	49.3	318	10	US-09-801-368-252 Sequence 252, App
8	749.5	48.6	386	10	US-09-734-569-170 Sequence 170, App
9	518	33.6	132	10	US-09-925-301-1459 Sequence 1459, Ap
10	423	27.4	87	10	US-09-864-761-36440 Sequence 36440, A
11	368	23.8	475	10	US-09-777-921A-4 Sequence 4, Appl1
12	368	23.8	477	10	US-09-777-921A-2 Sequence 2, Appl1
13	333.5	21.6	410	10	US-09-777-921A-5 Sequence 5, Appl1
14	314	20.3	469	9	US-09-992-598-289 Sequence 289, App
15	314	20.3	469	10	US-09-989-722-289 Sequence 289, App
16	314	20.3	469	10	US-09-989-723-289 Sequence 289, App
17	314	20.3	469	10	US-09-989-727-289 Sequence 289, App
18	314	20.3	469	10	US-09-989-727-289 Sequence 289, App
19	314	20.3	469	10	US-09-989-731-289 Sequence 289, App

20	314	20.3	469	10	US-09-989-732-289 Sequence 289, App
21	314	20.3	469	10	US-09-991-073-289 Sequence 289, App
22	314	20.3	469	10	US-09-990-442-289 Sequence 289, App
23	314	20.3	469	10	US-09-991-163-289 Sequence 289, App
24	314	20.3	469	10	US-09-993-604-289 Sequence 289, App
25	314	20.3	469	10	US-09-990-456-289 Sequence 289, App
26	314	20.3	469	10	US-09-989-721-289 Sequence 289, App
27	314	20.3	469	12	US-10-006-867-58 Sequence 58, Appl
28	309	20.0	342	10	US-09-777-921A-6 Sequence 6, Appl1
29	274.5	17.8	289	10	US-09-796-766-20 Sequence 20, Appl
30	265	17.2	312	10	US-09-734-134-2 Sequence 2, Appl1
31	265	17.2	312	10	US-09-826-507-2 Sequence 2, Appl1
32	265	17.2	312	10	US-09-808-457-2 Sequence 2, Appl1
33	264	17.1	310	9	US-10-042-194-1 Sequence 1, Appl1
34	257.5	16.7	309	10	US-09-884-814-8 Sequence 8, Appl1
35	257	16.7	131	10	US-09-925-300-1808 Sequence 1808, Ap
36	254.5	16.5	309	10	US-09-884-814-6 Sequence 1, Appl1
37	250.5	16.2	309	10	US-09-884-814-6 Sequence 6, Appl1
38	250	16.2	433	10	US-09-796-766-18 Sequence 18, Appl
39	246.5	16.0	323	12	US-10-006-867-126 Sequence 126, App
40	242	15.7	410	10	US-09-796-766-10 Sequence 10, Appl
41	241.5	15.7	275	10	US-09-808-457-4 Sequence 4, Appl1
42	240.5	15.6	436	10	US-09-796-766-21 Sequence 21, Appl
43	232.5	15.1	320	10	US-09-840-787-12 Sequence 12, Appl
44	222.5	14.4	300	10	US-09-810-673A-6 Sequence 6, Appl1
45	218	14.1	272	10	US-09-796-766-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-811-094-33
Sequence 33, Application US/09811094
Patent No. US20010044144A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Willey, Sandra Eileen
APPLICANT: Willey, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yazhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT'),
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811.094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-811-094-33
Query Match 100.0%; Score 1543; DB 10; Length 298;
Best Local Similarity 100.0%; Pred. No. 3 8e-152;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEQAISPAKDFLAGGIAAISKTAADVIEVKLLQVHASKQIADKQYKGIYDCIVR 60
DB 1 MTEQAISPAKDFLAGGIAAISKTAADVIEVKLLQVHASKQIADKQYKGIYDCIVR 60
QY 61 IPKEGVLSFWRGNANVIRYEPQALNFAKDKYKQIFLGVDKQHFQFMRPGNLSG 120
DB 61 IPKEGVLSFWRGNANVIRYEPQALNFAKDKYKQIFLGVDKQHFQFMRPGNLSG 120
QY 121 GAAGTSLCFYVPLDFATRIADVGKSGTEREFGSLDCLVKTGSGIRGLYGFSSVS 180
DB 121 GAAGTSLCFYVPLDFATRIADVGKSGTEREFGSLDCLVKTGSGIRGLYGFSSVS 180

Db	1	MTDAALSPAKDQFLAGGVAAMISKTAFAPIERVNLLDQVASHQNTADRKRIIDOCYR	60
Qy	61	IPKQGVLSFPRKGLNAVIRYPPQALNFAFKOKYKQIFGQYDKHTQFRRYFAGNLASG	120
Db	61	IPKQGVLSFPRKGLNAVIRYPPQALNFAFKOKYKQIFGQYDKHTQFRRYFAGNLASG	120
Qy	121	GAAGATSLCEFYPLDFAFRTRIADVDGKSGTEREERFGLDGLVITKSDGIRGLYQGFNS	180
Db	121	GAAGATSLCEFYPLDFAFRTRIADVDGKSGTEREERFGLDGLVITKSDGIRGLYQGFNS	180
Qy	181	VQGIIRRAAYFQGVYDPAKGLPCKMTHILVYSMILNQOTAAVAGVSYPEDFVRRMM	240
Db	181	VQGIIRRAAYFQGVYDPAKGLPCKMTHILVYSMILNQOTAAVAGVSYPEDFVRRMM	240
Qy	241	QSGRKGDIMYTGVCDCWKRIIFRDEGSKAFPKGAMSVNLRMGCGAFVLVYDELK	296
Db	241	QSGRKGDIMYTGVCDCWKRIARDEGSKAFPKGAMSVNLRMGCGAFVLVYDELK	296

```

RESULT 5
US-09-811-094-31
; Sequence 31, Application US/09611094
; Patent No. US20010044144A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Thomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yezlong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT)
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.42004
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 297
; TYPE: PRF
; ORGANISM: Homo sapien
; US-09-811-094-31

```

Query Match	89.8%	Score 1385.5;	DB 10;	Length 297;
Best Local Similarly	87.2%	Pred. No. 7.4e-136;		
Matches 260; Conservative	21;	Mismatches 16;	Indels 1;	Gaps 1;

[illegible]

```

US-09-810-644-31
; Sequence 31, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davys, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yashong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-31

```

Query Match	89.8%	Score 1385.5	DB 10	Length 297
Best Local Similarity	87.2%	Pred. No. 7.4e-136		
Matches	260	Conservative 21	Mismatches 16	Indels 1
				Gaps 1
Qy	1	MTEQAISFAKDLAGIAAIAISKTVAPVPIERKLLLOVHASKQIADAKQYGIYDCIVR	60	
	1			
	1			
Db	1	MGDHAMSFKLDPDLACAVAAVAASKTAVAPVPIERKLLLOVHASKQIASEQYGIIDCYVR	60	
Qy	61	IPKEGVLSFWRGNLNANVIRYPTQALNFAFKDKYKQIFLAGVDKHTQPMRYFAGNLASG	120	
	61			
Db	61	IPKEGVLSFWRGNLNANVIRYPTQALNFAFKDKYKQIFLAGVDKHTQPMRYFAGNLASG	120	
Qy	121	GAGATSLTCEVYPLDPARTRLAADYKGSCTEREFRGLDGLVYITKSDGIRGLYOGESVS	180	
	121			
Db	121	GAGATSLTCEVYPLDPARTRLAADYGR-AQREEFHGLDCLIIKIFKSDGLRGLYOGESVS	179	
Qy	181	VGGIIIRYRAAYRGVDTAKGMLPDKRNTHIVVSMIAQVTVAVAGVSTPDTVRRRMM	240	
	181			
Db	180	VGGIIIRYRAAYRGVDTAKGMLPDKRNTHIIFKSMIAQSVTVAGLSTPDTVRRRMM	239	
Qy	241	QSGRGAGDITMYGTVDCKIRFDREGKAFKFGAMSNVLRGNGAVLVLYDELKVI	298	
	241			
Db	240	QSGRGAGDITMYGTVDCKIRIADKAKKFEFGAMSNVLRGNGAVLVLYDELKVI	297	

```

RESULT 7
US-09-801-368-252
; Sequence 252, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Solie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fung
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801.368
; CURRENT FILING DATE: 2001-03-07

```

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

Query Match	49.3%;	Score 760.5;	DB 10;	Length 318;
Best Local Similarity	-53.7%;	Pred. No. 3.8e-71;		
Matches 159;	Conservative 42;	Mismatches 86;	Indels 9;	Gaps 5;

[illegible]

```

RESULT 8
US-09-734-569-170
; Sequence 170, Application US/09734569
; Patent No. US20020064816A1
; GENERAL INFORMATION:
; APPLICANT: Lerchl, Jens
; APPLICANT: Renz, Andreas
; APPLICANT: Ehrhardt, Thomas
; APPLICANT: Reinndl, Andreas
; APPLICANT: Cirpus, Petra
; APPLICANT: Bischoff, Friedrich
; APPLICANT: Frank, Markus
; APPLICANT: Freund, Annette
; APPLICANT: Duwenig, Elke
; APPLICANT: Schmidt, Ralf-Michael
; APPLICANT: Reski, Ralf
; TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved
; TITLE OF INVENTION: In the synthesis of carbohydrates
; FILE REFERENCE: BASF-NAE-1332-99-US
; CURRENT APPLICATION NUMBER: US/09/734,569
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/171,101
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.1/WordPerfect 6.1
; SEQ ID NO 170
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-734-569-170

```

Query Match	48.6%;	Score 749.5;	DB 10;	Length 386;
Best Local Similarity	53.4%;	Pred. No. 6.7e-70;		
Matches 157;	Conservative 44;	Mismatches 84;	Indels 9;	Gaps 5;

QY 7 SFAKDFLAGGIAAISKTA VAPIERVKLLLOV - HASKQIAADKQYKGI VDCIVRIPKEQ 65

Db	84	SEMTDFLGMGSAVSAVSTAAPAFIRVRYLLIIONODEMLKSGRLSHPHYGECEFSRTFVKE	143
Qy	66	GVLSFWFNGCNLANVRYRPTOLANFAFKDKXKQJFLGSGVDHTQFWRFAGNLASGGAGA	125
Db	144	GMSLMMGNLANVRIPTQALNFAFDYKSLFGYKKDK-DGYKKFAGNLASGGAGA	202
Qy	126	TSLCFYVPLDEFARTRLADV---GKSTEREERFRLGDCLVKITKSDGIRGLYGFVSVO	182
Db	203	SLSLFVYSLDVARFRLANDAKSSKKGGEROFNLVYRYKTLATDIAELYRGFALISCA	262
Qy	183	GIILYRAAYFEGVYTPAG-MLPDKRNHIYVSMIAOTVAVAGVVSPEDTYRRRMMQ	241
Db	263	GIYYRGILFEIYDLSKLPVVLVGLNEGNFLASFLLGIGITIGAGLASYPIDTVRRRRMMT	322
Qy	242	SGRGADIMTYGVDCWKRIFRDGGCAAFRGAMSNLRGAGAFVLYLVDELK	295
Db	323	SGEA---VKVNGSMDARQQLIARKGASLFGAGANTLLRAVAGVLSGTDQIQ	373

```

RESULT 9
US-09-925-301-1459
: Sequence 1459, Application US/09925301
: Patent No. US20020052308A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA106
: CURRENT APPLICATION NUMBER: US/09/925,301
: CURRENT FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05882
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 1694
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1459
: LENGTH: 132
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (115)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (123)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (126)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (129)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1459

```

Query Match	33.6%;	Score 518;	DB 10;	Length 132;
Best Local Similarity	96.3%;	Pred. No. 1.4e-46;		
Matches 103; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

QY	1	MTBEAIFAFADPFLAGGIAAISTANAPPIERKLLQYOHASKIADKQYKICIVCIYR	60
QY	26	MTBEAIFAFADPFLAGGIAAISTANAPPIERKLLQYOHASKIADKQYKICIVCIYR <td>85</td>	85
Db	61	IPKEQGVLSFWKGNLANVIRPEPQALNAFKDKKQKFLGCVYKHT	107
QY	86	IPKQGVLSFWKGNLANVIRPEPQALNAFKDKKQKFLGCVYKHT	132

```

RESULT 10
US-09-864-761-36440
; Sequence 36440, Application US/0986476
; Patent No. US20020048763A1
; GENERAL INFORMATION:

```


	Best Local	Similarity	32.7%	Pred. No.	2.6e-30,	
	Matches	97;	Conservative	60;	Mismatches	112;
					Indels	28;
					Gaps	10.
QY	10	KDFLAGIAAASKRAVAPIERVKLLLOAHASKIOAADKQYKGIYDCIVRIPIKEGVLS	69			
		: : : : : : : : : : : : : :				
Db	196	ROLLAGGIAGAAASRSTAPLDRKLTIMQY-HSKM--NIFGGRQWKEGIGS	249			
QY	70	FWRGLNAVIRYEPPOALNFAFKDKYKQIFLGVGDHHTQFWRYEAGNTLASGAAGATSLC	129			
		: : : : : : : : : : : : :				
Db	250	LWRGGRIVNIKIAPEFAKFMAYEEDYKKLLTEEGOKIGFEEFISGSM----ACATAQT	304			
QY	130	FVYPLDPARTRLAAVGVSGTEREERGGDCIVKTKSGISGIVGQESVSVOGIIYYA	189			
		: : : : : : : : : : : : :				
Db	305	FILPEHVKRRLA--VGKTG---QISGIIDCKAKKILKEGLAEPFKGVPNLIGIIPYG	359			
QY	190	AFEGYIDFAK-----GMLPDPKNTIIIVYSWMAQTAVYAGVSVYEPFDVRRRMQSGR	244			
		: : : : : : : : : : : : :				
Db	360	IDLAVYEELKSYWLDNFAKSDVNPQVMVLLGCGALSTSCGQLASYPALVRRIRMQQAAL	419			
QY	245	KGADIMYIGYDCAKKIRFDEGGKAFKFGAMSN---VLKMGGAFLVLYIDELKKYI	298			
		: : : : : : : : : : : : :				
Db	420	EGSPDL--NMWGLFRRIISKEGIPGLYKRIITPNFMKVIIPAVGISY--VYVENMKQTL	472			

RESULT 15
US-09-989-722-289
Sequence 289, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C63
CURRENT APPLICATION NUMBER: US/09/989,722
PRIOR APPLICATION NUMBER: 2001-11-19
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088555
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349

;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 20.3%; Score 314; DB 10; Length 469;
Best Local Similarity 30.1%; Pred. No. 9.9e-25;
Matches 89; Conservative 60; Mismatches 115; Indels 32; Gaps 11;

Oy 10 KDFLAGTAIASTKAVAPIERVKLLLOYHASKOIAADKOKYIVDCIVRKPEQVLS 69
Db 188 RHLVAGGAGAVSKTCTAPLDRLKVMOV-HASR-----SNMGIVGFTOMIREGARS 241
Oy 70 FWRGNLAVIRYFTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSGAGATSIC 129
Db 242 LMRGNGINVLRKAPESAIKFMAYEQIKR--LVGSDQET---LRHRLVAGSLAGAIAS 296
Oy 130 FVYPLDFAIRLADVSGSKTEREFRGLDCLVKTKSDGIRGLYOGFESVVOGIITRYRA 189
Db 297 SIYPMEVILKTRMA--LRKTG---QYSGMLDCARRILAREGVAAPYKGYVFNMLGITIPYAG 351

Oy 190 AFGYVDYAKGM-----LPDPKNTHLIVSMIAQPTAVAG--VSYPTFVRRMM 240
Db 352 IDLAVYETLKNAMLQHYAVNSADPG----VFVLLACGTWSSTCGQLASTPLALVTRMOA 407
Oy 241 QSGRGADIMYTGTVDCWRKIFRDEGKAFFKGANSVNLRGKGAFV--LVLYDELK 295
Db 408 QASIEGAPEVIMSSL--FKHLIRTEGAFGLYRGLAPNFMKVIPAVISISVYENLK 461

Search completed: November 12, 2002, 16:56:57
Job time : 7.34043 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:44:05 ; Search time 14.0157 Seconds
(without alignments)
2044.001 Million cell updates/sec

Title: US-09-393-441-33

Perfect score: 1543
Sequence: 1 MTEQAIISFAADFLAGGIAAA.....LRGKGAFVLYLDELKKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	1	S03894 ADP,ATP carrier pr
2	1512	98.0	298	2	B43646 ADP,ATP carrier pr
3	1454	94.2	298	1	A29132 ADP,ATP carrier pr
4	1424	92.3	298	1	I60173 adenine nucleotide
5	1422	92.2	298	1	KWBO ADP,ATP carrier pr
6	1418	91.9	298	2	S37210 ADP,ATP carrier pr
7	1409	91.3	298	1	A44778 ADP,ATP carrier pr
8	1405	91.1	298	1	S31814 ADP,ATP carrier pr
9	1184	76.7	301	1	S31935 ADP,ATP carrier pr
10	1041	67.5	313	2	T23207 hypothetical prote
11	1039	67.3	313	2	T25850 hypothetical prote
12	1038	67.3	300	2	T25371 hypothetical prote
13	993.5	64.4	300	2	T15206 hypothetical prote
14	978	63.4	339	2	A41677 ADP,ATP carrier pr
15	943	61.1	301	2	S51132 ADP,ATP carrier pr
16	778.5	50.5	307	2	A36582 ADP,ATP carrier pr
17	772	50.0	308	1	S30259 ADP,ATP carrier pr
18	769	49.8	322	2	T40526 edp/atp translocas
19	768	49.8	386	2	T09709 ADP,ATP carrier pr
20	766	49.6	313	1	KWNC ADP,ATP carrier pr
21	764	49.5	326	2	T25728 hypothetical prote
22	762.5	49.4	305	2	S68154 ADP,ATP carrier pr
23	760.5	49.3	318	1	A31978 ADP,ATP carrier pr
24	756.5	49.0	306	2	T20012 hypothetical prote
25	750	48.6	387	2	S14876 ADP,ATP carrier pr
26	748	48.5	386	2	S21974 ADP,ATP carrier pr
27	747	48.4	306	2	T42011 ADP,ATP carrier pr
28	747	48.4	386	2	S17917 ADP,ATP carrier pr
29	744	48.2	387	2	S16568 ADP,ATP carrier pr

30	743	48.2	379	2	T04608 ADP,ATP carrier pr
31	742.5	48.1	385	1	S29852 ADP,ATP carrier pr
32	742	48.1	382	2	S33630 ADP,ATP carrier pr
33	739.5	47.9	386	2	S14874 ADP,ATP carrier pr
34	737.5	47.8	309	2	A24849 ADP,ATP carrier pr
35	734.5	47.6	379	2	S21313 ADP,ATP carrier pr
36	681.5	44.2	298	2	T24029 hypothetical prote
37	520.5	33.7	327	2	T51577 ADP,ATP translocas
38	383	24.8	325	2	T04273 hypothetical prote
39	381	24.7	352	2	T01729 hypothetical solu
40	372	24.1	358	2	T45934 hypothetical prote
41	370.5	24.0	415	2	T48171 hypothetical prote
42	369.5	23.9	381	2	T51158 hypothetical prote
43	368	23.8	475	2	T50686 peroxisomal Ca-dep
44	363	23.5	348	2	D84798 probable mitochond
45	344.5	22.3	332	2	T47703 Ca-dependent solut

ALIGNMENTS

RESULT 1

S03894

ADP,ATP carrier protein T3 - human

N:Alternate names: ADP,ATP carrier protein T2 (misidentification): mitochondrial ADP, C:Species: Homo sapiens (man)

C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000 C:Accession: S03894; B28116

R:Cozens, A.L.; Runswick, M.J.; Walker, J.E. J. Mol. Biol. 206, 261-280, 1989

A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP A:Reference number: S03893; MUID:89236396; PMID:2541251

A:Accession: S03894

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-298 <CDS>

R:Howdsworth, J.; Attardi, G. Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1 A:Reference number: A94197; MUID:88124845; PMID:2829183

A:Accession: B28116

A:Molecule type: mRNA

A:Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>

A:Cross-references: GB:J03392; NID:9339722; PIDN:AAA36750.1; PID:9339723

A:Experimental source: Liver

C:Genetics:

A:Gene: GDB:ANT3; ANT3Y

A:Cross-references: GDB:125184; OMIM:300151; OMIM:403000

A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3

A>Note: There may be some confusion in the assignment of sequences for GDB:ANT2 and G C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein F:2-298/Product: ADP,ATP carrier protein repeat predicted <ANT>

F:5-99/Domains: ADP,ATP carrier protein repeat homology <ACP1>

F:110-202/Domains: ADP,ATP carrier protein repeat homology <ACP2>

F:207-298/Domains: ADP,ATP carrier protein repeat homology <ACP3>

Query Match

Best Local Similarity 100.0%; Score 1543; DB 1; Length 298; Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTEQAIISFAKDFLAGGIAAAISKTVAPEERKLLQVHASKQIAADKQYGYDCTVR	60
DB	1	MTEQAIISFAKDFLAGGIAAAISKTVAPEERKLLQVHASKQIAADKQYGYDCTVR	60
QY	61	IRKEGVSEFMGNANVIRYPTQALNFAFDKXKQIFLGGVDKHQFWRFAAGNLASG	120
DB	61	IRKEGVSEFMGNANVIRYPTQALNFAFDKXKQIFLGGVDKHQFWRFAAGNLASG	120
QY	121	GAAGATSLCFVYPPLDFARTRLAADVGKSGTEREFGDLGVKIRKSDGIRGLYOGFSVS	180
DB	121	GAAGATSLCFVYPPLDFARTRLAADVGKSGTEREFGDLGVKIRKSDGIRGLYOGFSVS	180

QY 181 VGGIIIRAAVFGYVDFAKGMLDPKNTHTVSMIAQVTAAGVSYPPDVTYRRMM 240
 |||||
 Db 181 VGGIIIRAAVFGYVDFAKGMLDPKNTHTVSMIAQVTAAGVSYPPDVTYRRMM 240
 QY 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFFKGMNVLRGMGAFVLYLYDELKVI 298
 |||||
 Db 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFFKGMNVLRGMGAFVLYLYDELKVI 298

RESULT 2

B43646
 ADP/ATP carrier protein T2 - bovine

C:Species: Bos primigenius taurus (cattle)
 C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
 C:Accession: B43646

R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989

A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093; PMID:2540808

A:Accession: B43646
 A:Molecule type: mRNA
 A>Status: preliminary

A:Residues: 1-298 <POM>
 A:Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology

C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPi>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 98.0%; Score 1512; DB 2; Length 298;
 Best Local Similarity 97.7%; Pred. No. 3.6e-126;
 Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTEBAISFANDFLAGIAAISKTAAPVIERVKLLQVHASKQIADKQYKGIIVDCIVR 60
 |||||
 Db 1 MTEBAISFANDFLAGIAAISKTAAPVIERVKLLQVHASKQIADKQYKGIIVDCIVR 60
 QY 61 IPKEQGVLSFWRGNLANVIRYFPQALNFAFKDKYKQIFLGVDKHTQFWRVFNAGNLASG 120
 |||||
 Db 61 IPKEQGVLSFWRGNLANVIRYFPQALNFAFKDKYKQIFLGVDKHTQFWRVFNAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFKARTRLADVKGSGTEREFGIGDCLVTKTSGDGRIGLYOGFSVS 180
 |||||
 Db 121 GAAGATSLCFVYPLDFKARTRLADVKGSGTEREFGIGDCLVTKTSGDGRIGLYOGFSVS 180
 QY 181 VGGIIIRAAVFGYVDFAKGMLDPKNTHTVSMIAQVTAAGVSYPPDVTYRRMM 240
 |||||
 Db 181 VGGIIIRAAVFGYVDFAKGMLDPKNTHTVSMIAQVTAAGVSYPPDVTYRRMM 240
 QY 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFFKGMNVLRGMGAFVLYLYDELKVI 298
 |||||
 Db 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFFKGMNVLRGMGAFVLYLYDELKVI 298

RESULT 3

A29132
 ADP/ATP carrier protein T2 - human

N:Alternate names: mitochondrial ADP/ATP translocase 2
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000

C:Accession: A29132; C28116
 R:Ballini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
 J. Biol. Chem. 262, 4355-4359, 1987

A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulated
 A:Reference number: A29132; MUID:87160056; PMID:3031073

A:Accession: A29132
 A:Molecule type: mRNA
 A:Residues: 1-298 <BAT>

A:Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
 R:Shouldsworth, J.; Altardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

*A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a

A:Reference number: A94197; MUID:88124845; PMID:2829183
 A:Accession: C28116
 A:Molecule type: mRNA
 A:Residues: 47-65, 'C', 67-110, 'L', 112-161, 'G', 163-298 <HOU>
 A:Cross-references: GB:J03591; NID:g339720; PIDN:AAA56749.1; PID:g339721
 A:Experimental source: clone pHA73
 C:Genetics:
 A:Gene: GDB:ANT2; T3; 2F1

A:Cross-references: GDB:125190; OMIM:300150
 A:Map position: Xq13-Xq26

A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPi>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1454; DB 1; Length 298;
 Best Local Similarity 92.6%; Pred. No. 4.9e-121;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEBAISFANDFLAGIAAISKTAAPVIERVKLLQVHASKQIADKQYKGIIVDCIVR 60
 |||||
 Db 1 MTEBAISFANDFLAGIAAISKTAAPVIERVKLLQVHASKQIADKQYKGIIVDCIVR 60
 QY 61 IPKEQGVLSFWRGNLANVIRYFPQALNFAFKDKYKQIFLGVDKHTQFWRVFNAGNLASG 120
 |||||
 Db 61 IPKEQGVLSFWRGNLANVIRYFPQALNFAFKDKYKQIFLGVDKHTQFWRVFNAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFKARTRLADVKGSGTEREFGIGDCLVTKTSGDGRIGLYOGFSVS 180
 |||||
 Db 121 GAAGATSLCFVYPLDFKARTRLADVKGSGTEREFGIGDCLVTKTSGDGRIGLYOGFSVS 180
 QY 181 VGGIIIRAAVFGYVDFAKGMLDPKNTHTVSMIAQVTAAGVSYPPDVTYRRMM 240
 |||||
 Db 181 VGGIIIRAAVFGYVDFAKGMLDPKNTHTVSMIAQVTAAGVSYPPDVTYRRMM 240
 QY 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFFKGMNVLRGMGAFVLYLYDELKVI 298
 |||||
 Db 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFFKGMNVLRGMGAFVLYLYDELKVI 298

RESULT 4

I60173
 adenine nucleotide translocator - rat

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
 C:Accession: I60173

R:Shimohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
 Biochim. Biophys. Acta 1152, 192-196, 1993

A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding r
 A:Reference number: I60173; MUID:94002161; PMID:8399300

A:Accession: I60173
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-298 <RES>

A:Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA43842.1; PID:g400427
 C:Genetics:
 A:Gene: anti1

A:Introns: 37/3; 200/1; 247/1
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACPi>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 92.3%; Score 1424; DB 2; Length 298;
 Best Local Similarity 89.6%; Pred. No. 2.2e-118;
 Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEBAISFANDFLAGIAAISKTAAPVIERVKLLQVHASKQIADKQYKGIIVDCIVR 60
 |||||
 Db 1 MTEBAISFANDFLAGIAAISKTAAPVIERVKLLQVHASKQIADKQYKGIIVDCIVR 60

QY 61 IPKEGVLSFWMGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKHTQPMRFAGNLASG 120
 |||||
 Db 61 IPKEGVLSFWMGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKHTQPMRFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADYGVKSGTEREFGGLDCLVTKIRKSDIRGLYOGFSVS 180
 |||||
 Db 121 GAAGATSLCFVYPLDFARTRLADYGVKSGTEREFGGLDCLVTKIRKSDIRGLYOGFSVS 180
 QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTIIVYSMMIAQTVTAVAGVSPFDTVRRMM 240
 |||||
 Db 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTIIVYSMMIAQSVTAVAGVSPFDTVRRMM 240
 QY 241 OSGRKGADIMYGTVDCKMRKIRDEGKAFKFGAMSNVLRGGAFAVLVYDELKKVI 298
 |||||
 Db 241 OSGRKGADIMYGTVDCKMRKIRAKDEGKRAFFKGAAMSNVLRGGAFAVLVYDEIRKVV 298

RESULT 5

XMB0

ADP/ATP carrier protein T1 - bovine
 N:Alternate names: ADP/ATP translocase T1
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 14-Nov-1993 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999
 C:Accession: A43646; A24822; A03181; A61343; S69369
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093; PMID:2540808
 A:Accession: A43646
 A:Molecule type: mRNA
 A:Residues: 1-298 <POM>
 A:Cross-references: GB:M4102; NID:9529414; PIDN:AAA30768.1; PID:9529415
 R:Rasmussen, U.B.; Wohlitz, H.
 Biochem. Biophys. Res. Commun. 138, 850-857, 1986
 A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual
 A:Reference number: A24822; MUID:86295775; PMID:3017341
 A:Accession: A24822
 A:Molecule type: mRNA
 A:Residues: 208-298 <RAS>
 A:Cross-references: GB:M43783; NID:9162630; PIDN:AAA30363.1; PID:9162631
 R:Aquila, H.; Mistr, D.; Eulitz, M.; Klingenberg, M.
 Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
 A:Title: Complete amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondria
 A:Reference number: A03181; MUID:82188267; PMID:7076130
 A:Accession: A03181
 A:Molecule type: Protein
 A:Residues: 2-51, 'X', '53-70', 'X', '72-109', 'X', '111-298 <AOU>
 A:Note: residue 52 may be methyllysine
 R:Babel, W.; Wachter, E.; Aquila, H.; Klingenberg, M.
 Biochim. Biophys. Acta 670, 176-180, 1981
 A:Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondria
 A:Reference number: A61343; MUID:82046808; PMID:6271240
 A:Accession: A61343
 A:Molecule type: protein
 A:Residues: 205-298 <BAB>
 R:Oetmeier, W.; Masson, K.; Kalina, S.
 Eur. J. Biochem. 227, 730-733, 1995
 A:Title: [(3)H]-7-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP
 A:Reference number: S69369; MUID:95172058; PMID:7867632
 A:Accession: S69369
 A:Molecule type: protein
 A:Residues: 49-63,154-168 <OET>
 C:Comment: This protein is synthesized in the cytosol and transported into the mitochondrion
 C:Complex: homodimer
 C:Function:
 A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
 A:Note: located in the inner mitochondrial membrane
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitoch
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACF1>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACF3>

F:2/Modified site: acetylated amino end (Ser) (1n mature form) #status experimental
 F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 92.2%; Score 1422; DB 1; Length 298;

Best Local Similarity 89.3%; Pred. No. 3.3e-118;

Matches 266; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQAIISPAKDFLAGIAAISKTAVERKLLQVOHASKQIAADKQYGYDCTYR 60
 |||||
 Db 1 MSDQALSFLEKDFLAGIAAISKTAVERKLLQVOHASKQISAEQYGGIIDCVRR 60
 QY 61 IPKEGVLSFWMGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKHTQPMRFAGNLASG 120
 |||||
 Db 61 IPKEGVLSFWMGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKHTQPMRFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADYGVKSGTEREFGGLDCLVTKIRKSDIRGLYOGFSVS 180
 |||||
 Db 121 GAAGATSLCFVYPLDFARTRLADYGVKGAQREFGLGCLVTKIRKSDIRGLYOGFSVS 180
 QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTIIVYSMMIAQTVTAVAGVSPFDTVRRMM 240
 |||||
 Db 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTIIVYSMMIAQSVTAVAGVSPFDTVRRMM 240
 QY 241 OSGRKGADIMYGTVDCKMRKIRDEGKAFKFGAMSNVLRGGAFAVLVYDELKKVI 298
 |||||
 Db 241 OSGRKGADIMYGTVDCKMRKIRAKDEGKRAFFKGAAMSNVLRGGAFAVLVYDEIRKVV 298

RESULT 6

S37210

ADP/ATP carrier protein T1 - mouse

N:Alternate names: adenine nucleotide carrier

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999

C:Accession: S37210

R:Laplace, C.; Costet, P.

submitted to the EMBL Data Library, September 1993

A:Reference number: S37210

A:Accession: S37210

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-298 <LAP>

A:Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628

C:Genetics: ANCI

C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACF1>

F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACF2>

F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACF3>

Query Match 91.9%; Score 1418; DB 2; Length 298;

Best Local Similarity 88.9%; Pred. No. 7.6e-118;

Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTEQAIISPAKDFLAGIAAISKTAVERKLLQVOHASKQIAADKQYGYDCTYR 60
 |||||
 Db 1 MSDQALSFLEKDFLAGIAAISKTAVERKLLQVOHASKQISAEQYGGIIDCVRR 60
 QY 61 IPKEGVLSFWMGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKHTQPMRFAGNLASG 120
 |||||
 Db 61 IPKEGVLSFWMGNLANVIRYPTQALNPAFKDKYKQIFLGGVDKHTQPMRFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADYGVKSGTEREFGGLDCLVTKIRKSDIRGLYOGFSVS 180
 |||||
 Db 121 GAAGATSLCFVYPLDFARTRLADYGVKSGSSQREFGLDCLVTKIRKSDIRGLYOGFSVS 180
 QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTIIVYSMMIAQTVTAVAGVSPFDTVRRMM 240
 |||||
 Db 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTIIVYSMMIAQSVTAVAGVSPFDTVRRMM 240
 QY 241 OSGRKGADIMYGTVDCKMRKIRDEGKAFKFGAMSNVLRGGAFAVLVYDELKKVI 298
 |||||

Db 241 QSGRKGADIMYGTGTLDCWKRIADDEGANAEEFKGAMSNVLRGMGAFVLYLDEIKRYV 298

RESULT 7

ADP,ATP carrier protein T1 - human

N:Alternate names: mitochondrial ADP,ATP translocase 1

C:Species: Homo sapiens (man)

C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000

C:Accession: A44778; S03893; A39891; A28116

R:Li, K.; Warner, C.K.; Hodges, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.

J. Biol. Chem. 264, 13998-14004, 1989

A:Title: A human muscle adenine nucleotide translocator gene has four exons, is located

A:Reference number: A44778; M0ID:89340499; PMID:2547778

A:Accession: A44778

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-298 <L1A>

A:Cross-references: GB:J04982; NID:g178658; PIDN:AAA51736.1; PID:g178659

R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.

J. Mol. Biol. 206, 261-280, 1989

A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr

A:Reference number: S03893; M0ID:89226396; PMID:2541251

A:Accession: S03893

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-298 <COZ>

R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.

Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987

A:Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader

A:Reference number: A39891; M0ID:88041149; PMID:2823266

A:Accession: A39891

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-15 'A', 17-146 'RR', 149, 151-226 'L', 228-298 <NEC>

A:Cross-references: GB:J02866; NID:g3339919; PIDN:AAA61223.1; PID:g333920

A:Experimental source: clone PHMAF

R:Houldsworth, J.; Attardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in d

A:Reference number: A94197; M0ID:88124845; PMID:2829183

A:Accession: A28116

A:Molecule type: mRNA

A:Residues: 1-37 <HOU>

A:Cross-references: GB:J03593; NID:g3339724; PIDN:AAA36751.1; PID:g333925

A:Experimental source: liver

C:Genetics:

A:Gene: GDB:ANT1, T1

A:Cross-references: GDB:119680; OMIM:103220

A:Map position: 4q35-4q35

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein

F:2-298/Product: ADP,ATP carrier protein #status predicted <MAT>

F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACPI>

F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACPI>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACPI>

Query Match 91.3%; Score 1409; DB 1; Length 298;
Best Local Similarity 88.3%; Pred. No. 4,7e-117;
Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTEQALSFANDFLAGIAAISKTAAPRIERVKLLLOVHASKQIADKQYKIVDCIVR 60
Db 1 MGDHAWSEFLDGLAGVAAANSTAVAPIERVKLLLOVHASKQISAEKQYKGIIDCVR 60

QY 61 IPKQGVLSFWRGNLANVIRFPTQALNFAFKKQYKQIFLGVDVKHGFWRYPAGNLASG 120
Db 61 IPKQGVLSFWRGNLANVIRFPTQALNFAFKKQYKQIFLGVDVKHGFWRYPAGNLASG 120

QY 121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFGGLDCLVTKSGDGLKYGQFSVS 180
Db 121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFGGLDCLVTKSGDGLKYGQFSVS 180

QY 181 VGGIIYRAAYFGVYDTAKGMLPDPKNTHTLVSMWIAQVTAAGVVSYPEDVRRMM 240
Db 181 VGGIIYRAAYFGVYDTAKGMLPDPKNTHTLVSMWIAQSVTAAGVVSYPEDVRRMM 240

QY 241 QSGRKGADIMYGTGTLDCWKRIADDEGAKAFKGAWSNVLRGMGAFVLYLDEIKRYV 298
Db 241 QSGRKGADIMYGTGTLDCWKRIADDEGAKAFKGAWSNVLRGMGAFVLYLDEIKRYV 298

RESULT 8

ADP,ATP carrier protein T2 - mouse

N:Alternate names: adenine nucleotide translocase

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998

C:Accession: S31814

R:Costet, P.; Laplace, C.

submitted to the EMBL Data Library, January 1993

A:Reference number: S31814

A:Accession: S31814

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-298 <COS>

A:Cross-references: EMBL:X70847

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACPI>

F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACPI>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACPI>

Query Match 91.1%; Score 1405; DB 2; Length 298;
Best Local Similarity 89.2%; Pred. No. 1.1e-116;
Matches 264; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTEQALSFANDFLAGIAAISKTAAPRIERVKLLLOVHASKQIADKQYKIVDCIVR 60
Db 1 MTEQALSFANDFLAGVAAANSTAVAPIERVKLLLOVHASKQISAEKQYKGIIDCVR 60

QY 61 IPKQGVLSFWRGNLANVIRFPTQALNFAFKKQYKQIFLGVDVKHGFWRYPAGNLASG 120
Db 61 IPKQGVLSFWRGNLANVIRFPTQALNFAFKKQYKQIFLGVDVKHGFWRYPAGNLASG 120

QY 121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFGGLDCLVTKSGDGLKYGQFSVS 180
Db 121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFGGLDCLVTKSGDGLKYGQFSVS 180

QY 181 VGGIIYRAAYFGVYDTAKGMLPDPKNTHTLVSMWIAQVTAAGVVSYPEDVRRMM 240
Db 181 VGGIIYRAAYFGVYDTAKGMLPDPKNTHTLVSMWIAQSVTAAGVVSYPEDVRRMM 240

QY 241 QSGRKGADIMYGTGTLDCWKRIADDEGAKAFKGAWSNVLRGMGAFVLYLDEIKRYV 296
Db 241 QSGRKGADIMYGTGTLDCWKRIADDEGAKAFKGAWSNVLRGMGAFVLYLDEIKRYV 296

RESULT 9

ADP,ATP carrier protein - African malaria mosquito

C:Species: Anopheles gambiae (African malaria mosquito)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S31935; S31936

R:Beard, C.B.; Crews-Owen, A.E.; Collins, F.H.

submitted to the EMBL Data Library, February 1993

A:Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae

A:Reference number: S31935

A:Accession: S31935

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-301 <BEA>

A:Cross-references: EMBL:Z21814; EMBL:Z21815

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:7-101/Domain: ADP,ATP carrier protein repeat homology <ACPI>

Db 8 NFADEFLMGISAIISKVVPPIERVKMLIQODSIPETIKSGOVERYSGLINCFFKRVSK 67
Qy 65 OCVLSFWKGNLANVIRYFTQALNFAEKDKYKOIFLGVDKHTOFWRFFAGNLASGANG 124
Db 68 OCVLSIMRGVNANVIRYFTQAENFAFKDYFNIF-PRYDQNTDFSKFCVNILSGATAG 126
Qy 125 ATSLCEVYPPLDFARTRLADVGKSGTEREFRGLGDCLVKITKSDGIRGLYOGFSYSVOGI 184
Db 127 AISLIVIPPLDFARTRLASDICK-GKDRQFTGLFDCLAKIKOTGLLSYSGFVSVTGI 185
Qy 185 IYRAAYEGVYDTAKGML-PDPKNTIYVSNMIAQTVTAAGVSYPEFTVRRMMMSG 243
Db 186 IYRGSYFGLYDSAKALFTNDKNTNIVLKMAVAOSVTILAGLISYPEFTVRRMMMSG 245
Qy 244 RKG-ADIMYTGIVDCRKIFRDEGKAFKFGKAMSNVLRGMGAFVLYLYDELKVI 298
Db 246 RKGEEIOYKNTIDCMIKILRNEGFGFKGAMANYIRGAGALVLYFYDELOKLI 301

Search completed: November 12, 2002, 16:48:38
Job time : 15.0157 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:43:20 : Search time 7.67525 Seconds
(without alignments)
1610.364 Million cell updates/sec

Title: US-09-393-441-33

Perfect score: 1543

Sequence: 1 MTEQAISFAKFLAGGIAA.....LRGNGAFVLYDELRKVI 298

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SWISSProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1543	100.0	298	ADP3_HUMAN	P12236 homo sapien
2	1512	98.0	298	ADP3_BOVIN	P32007 bos taurus
3	1463	94.8	298	ADP2_HUMAN	P05141 homo sapien
4	1451	94.0	298	ADP2_RAT	P09073 rattus norv
5	1445	93.6	298	ADP2_MOUSE	P51861 mus musculu
6	1424	92.3	298	ADP1_RAT	P05862 rattus norv
7	1418	91.9	298	ADP1_MOUSE	P48962 mus musculu
8	1417	91.8	297	ADP1_BOVIN	P02722 bos taurus
9	1409	91.3	298	ADP1_HUMAN	P12235 homo sapien
10	1217.5	78.9	297	ADP_ANCE	P26365 drosophila
11	1204	78.0	301	ADP_ANCE	P27238 anopheles g
12	978	63.4	339	ADP_CHLKE	P31692 chlorella k
13	778.5	50.5	307	ADP3_YEAST	P18238 saccharomyc
14	772	50.0	308	ADP_CHLRE	P27080 chlamydomon
15	769	49.8	322	ADP_SCHPO	P09188 schizosacch
16	768	49.8	386	ADP1_GOSHI	P02342 gossypium h
17	766	49.6	313	ADP_NEUCR	P02723 neurospora
18	762.5	49.4	305	ADP_KUDLA	P49382 kluyveromyc
19	760.5	49.3	318	ADP2_YEAST	P18239 saccharomyc
20	750.5	48.6	385	ADP2_ARATH	P40941 arabidopsis
21	750	48.6	387	ADP1_MAIZE	P04709 zea mays (m
22	748	48.5	386	ADP1_SOLTU	P25683 solanum tub
23	747	48.4	382	ADP_ORYSA	P16591 oryza sativ
24	744	48.2	387	ADP2_MAIZE	P12857 zea mays (m
25	742.5	48.1	381	ADP1_ARATH	P31167 arabidopsis
26	740	48.0	331	ADP1_WHEAT	P41629 triticum ae
27	739.5	47.9	386	ADP2_SOLTU	P27081 solanum tub
28	737.5	47.8	309	ADP1_YEAST	P04710 saccharomyc
29	727	47.1	331	ADP2_WHEAT	P41630 triticum ae
30	302	19.6	588	CMC2_CAEEL	P02099 caenorhabdi
31	300	19.4	330	GDC_BOVIN	P01888 bos taurus
32	299	19.4	307	ODC2_YEAST	P09297 saccharomyc
33	297	19.2	587	CMC3_CAEEL	P19529 caenorhabdi

34	295	19.1	678	1	CMC1_HUMAN	O75746 homo sapien
35	289.5	18.8	322	1	GDC_RAT	P16261 rattus norv
36	287.5	18.6	702	1	CMC1_CAEEL	O21153 caenorhabdi
37	286	18.5	325	1	UCP5_HUMAN	O95258 homo sapien
38	285	18.5	332	1	GDC_HUMAN	P16260 homo sapien
39	284	18.4	325	1	UCP5_MOUSE	O94282 mus musculu
40	282.5	18.3	326	1	YE08_SCHPO	O13805 schizosacch
41	280	18.1	675	1	CMC2_HUMAN	O94390 homo sapien
42	272	17.6	315	1	MPT_HUMAN	O912d1 homo sapien
43	270	17.5	315	1	SA18_HUMAN	O9h1k4 homo sapien
44	265	17.2	312	1	UCP3_HUMAN	P55916 homo sapien
45	265	17.2	676	1	CMC2_MOUSE	O9qxx4 mus musculu

ALIGNMENTS

```

RESULT 1
ADP3_HUMAN
ID ADP3_HUMAN STANDARD: PRT: 298 AA.
AC P12236; 096C49;
DT 01-OCT-1989 (Rel. 12, Created)
DR 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP, ATP carrier protein, liver isoform P2 (ADP/ATP translocase 3)
DE (Adenine nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89236396; PubMed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
RT ADP/ATP translocase."
RL J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhou J., Yu W., Tang H., Mel G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
RA Margolin J.F.;
RT Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RT Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 36-298 FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houdsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RT Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
RN [5]
RP FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
RP MITOCHONDRIAL INNER MEMBRANE.
RN [6]
RP SUBUNIT: HOMODIMER.
RN [7]
RP SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
RP inner membrane.
RN [8]
RP -I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
RN [9]
RP -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
RN [10]
RP This SWISS-PROT entry is copyright. It is produced through a collaboration
RP between the Swiss Institute of Bioinformatics and the EMBL outstation -
RP the European Bioinformatics Institute. There are no restrictions on its
RP use by non-profit institutions as long as its content is in no way
RP modified and this statement is not removed. Usage by and for commercial
RP entities requires a license agreement (See http://www.isb-sib.ch/announce/
RP or send an email to license@sib-sib.ch).
RN [11]
RP EMBL: J03592; AAA36750.1; -.

```


DE ADP,ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 GN (Adenine nucleotide translocator 2) (ANT 2).
 GN SLC25A5 OR ANT2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=90375457; PubMed=2168878;
 RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga F., Muzzel J.;
 RT "The human fibroblast adenine nucleotide translocator gene. Molecular
 cloning and sequence.";
 RL J. Biol. Chem. 265:16060-16063(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87166056; PubMed=3031073;
 RA Battini R., Ferrarri S., Kaczmarek L., Calabretta B., Chen S.T.,
 RT Baserga R.;
 RL "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
 growth-regulated.";
 RT J. Biol. Chem. 262:4355-4358(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Chen C.N., Su Y., Baybayan P., Siruno A., Nagataja R.,
 RA Mazzarella R.A., Schlessinger D., Chen E.Y.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Becker M., Graves T., Ozerky P.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 47-298 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houdsworth J., Altardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: M57424; AA51737.1; -
 DR EMBL: J02683; AA35379.1; -
 DR EMBL: L78810; AA83926.1; -
 DR EMBL: AC004000; AAB96347.1; -
 DR EMBL: J03591; AAA36749.1; -
 DR PIR: A29133; A29132.
 DR PIR: C28116; C28116.
 DR Genem; HGNC:10991; SLC25A5.
 DR MIM: 300150; -
 DR InterPro: IPR002067; MLC_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr_3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).

FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 6 6 V -> L (IN REF. 2).
 FT CONFLICT 66 66 G -> E (IN REF. 2).
 FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
 FT CONFLICT 162 162 V -> G (IN REF. 5).
 SQ SEQUENCE 298 AA: 32895 MW: F973C3AED92C49D3 CR64;
 Query Match 94.8%; Score 1463; DB 1; Length 298;
 Best Local Similarity 92.9%; Pred. No. 6; 9e-123;
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MPEQALSFAPKPLAGIAAISTATAPTEPVKLLQVQHASQIADKQYGVDCIVR 60
 DB 1 MPEQALSFAPKPLAGIAAISTATAPTEPVKLLQVQHASQIADKQYGVDCIVR 60
 QY 61 IPEQGVLSFMRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFMRFFAGNLAG 120
 DB 61 IPEQGVLSFMRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFMRFFAGNLAG 120
 QY 121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFGSLGCLVYTKSDGIRGLYGFYSV 180
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGKSGTEREFGSLGCLVYTKSDGIRGLYGFYSV 180
 QY 181 VGGIIYRAAYRGVDTAGMLPDPKNTHTVYSWMTAOTVTVAGVSVPEQVRRRMM 240
 DB 181 VGGIIYRAAYRGVDTAGMLPDPKNTHTVYSWMTAOTVTVAGVSVPEQVRRRMM 240
 QY 241 QSGRKADIMYGTVDCKRIKFEDEGKAFKFGKANSVLRGMCAGVLYLYDELKK 296
 DB 241 QSGRKADIMYGTVDCKRIKFEDEGKAFKFGKANSVLRGMCAGVLYLYDELKK 296
 RESULT 4
 ID ADP2_RAT STANDARD; PRT; 298 AA.
 AC 009073;
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP,ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 DE (Adenine nucleotide translocator 2) (ANT 2).
 GN SLC25A5 OR ANT2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shiohara Y., Kamida M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 encoding rat mitochondrial adenine nucleotide translocator.";
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 inner membrane.
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
 SKELETAL MUSCLE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D12771; BA02238.1; -.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987EFE35 CRC64;
 Query Match 94.0%; Score 1451; DB 1; Length 298;
 Best Local Similarity 91.9%; Pred. No. 8e-122;
 Matches 272; Conservative 15; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTEQAISFADFLAGIAAISKTAIVAPIERVKLLQVQHASKQIAADKQKGIIVDCIVR 60
 DB 1 MTDAAVSPADFLAGVAAASKTAIVAPIERVKLLQVQHASKQITADKQKGIIDCVVR 60
 QY 61 IPKEQGLSEWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVKHTQFWRFFAGNLASG 120
 DB 61 IPKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVKHTQFWRFFAGNLASG 120
 QY 121 GAAGATSLCEFYPLDFARTRLADVYKSGTEREFGDGLVTKTSDGIRGLYQGFVS 180
 DB 121 GAAGATSLCEFYPLDFARTRLADVYKSGTEREFGDGLVTKTSDGIRGLYQGFVS 180
 QY 181 VQGIITRAAFVGYDTRAKGMLPDKNTHTVSMIAQTVAAGVSYPRDYRRRRMM 240
 DB 181 VQGIITRAAFVGYDTRAKGMLPDKNTHTVSMIAQTVAAGVSYPRDYRRRRMM 240
 QY 241 QSGRKGADIMTGTVDCKRKIFRDEGKAFKFGKAMSNVLRGMSGAFVLYLDELKK 296
 DB 241 QSGRKGADIMTGTVDCKRKIFRDEGKAFKFGKAMSNVLRGMSGAFVLYLDELKK 296
 RESULT 5
 ADT2_MOUSE STANDARD; PRT; 298 AA.
 ID ADT2_MOUSE
 AC P51881; 061311;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP,ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 DE (Adenine nucleotide translocator 2) (ANT 2).
 GN SLC25A5 OR ANT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=97059403; Pubmed=8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse
 RT homologs";
 RL Mamm. Genome 7:25-30(1996).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA Sheldon J.G.;
 RL Thesis (1995), University of Cambridge, U.K.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RA Costet P., Laplace C.;
 RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP REVISIONS.
 RA Laplace C.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20432087; Pubmed=10974536;
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 RT translocase 1 and 2 genes.";
 RL Gene 254:57-66(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC Inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U27316; AAC52838.1; -.
 DR EMBL: U10404; AA119009.1; -.
 DR EMBL: X70847; CA450196.1; -.
 DR EMBL: AF240003; AAF64471.1; -.
 DR MGD: MGI:1353496; SLC25a5.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32931 MW; 079804B987EFE20 CRC64;
 Query Match 93.6%; Score 1445; DB 1; Length 298;
 Best Local Similarity 91.6%; Pred. No. 2.7e-121;
 Matches 271; Conservative 15; Mismatches 10; Indels 0; Gaps 0;
 QY 1 MTEQAISFADFLAGIAAISKTAIVAPIERVKLLQVQHASKQIAADKQKGIIVDCIVR 60
 DB 1 MTDAAVSPADFLAGVAAASKTAIVAPIERVKLLQVQHASKQITADKQKGIIDCVVR 60
 QY 61 IPKEQGLSEWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVKHTQFWRFFAGNLASG 120
 DB 61 IPKQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVKHTQFWRFFAGNLASG 120
 QY 121 GAAGATSLCEFYPLDFARTRLADVYKSGTEREFGDGLVTKTSDGIRGLYQGFVS 180
 DB 121 GAAGATSLCEFYPLDFARTRLADVYKSGTEREFGDGLVTKTSDGIRGLYQGFVS 180

DB 121 GAAGATSLCFVYPLDFARTRLADYGVKAGAREPFKGLGDCLVKIKYKSDGKIKLYOGFNS 180
QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTIIVYSMIAQTVTAAGVSYPFDTVRRMM 240
DB 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTIIVYSMIAQSVTAAGVSYPFDTVRRMM 240
QY 241 OSGRKGADIMYGTVDWCWKIRFDEGKAFKFGAMSNVLRGAGAVLVLYDEIKV 296
DB 241 OSGRKGADIMYGTVDWCWKIRFDEGKAFKFGAMSNVLRGAGAVLVLYDEIKV 296

RESULT 6
ADP1_MOUSE
ID ADP1_MOUSE STANDARD: PRT: 298 AA.
AC 005962;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (adenine nucleotide translocator 1) (ANT 1).
GN SL25A4 OR AN1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shinozuka Y., Kamida M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone encoding rat mitochondrial adenine nucleotide translocator.",
RL Biochim. Biophys. Acta 1152:192-196(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER EXTENT, IN BRAIN AND KIDNEY.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation in the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X61667; CAA43842.1; -;
DR EMBL: D12770; BAA02237.1; -;
DR InterPro: IPR002067; MLC_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA: 32969 MM: 66704FF78C6BC320 CRC64:

Query Match 92.3%; Score 1424; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 2e-119;

Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;
QY 1 MFEQATSEAKDPLAGIAAIAISTAVAPIERVKLLQVOHASKQIAADKQYGIYDCIVR 60
DB 1 MCDQALSFKDEFLAGIAAASVTAAPVPIERVKLLQVOHASKQIAAEKQYGIIDCVVR 60
QY 61 IRKEGVISFMWGNLANVIRYFPTQALNFAFDKYKOIFLGVDKTKQWRPAGLALSG 120
DB 61 IRKEGVISFMWGNLANVIRYFPTQALNFAFDKYKOIFLGVDKTKQWRPAGLALSG 120
QY 121 GAAGATSLCFVYPLDFARTRLADYGVKAGAREPFKGLGDCLVKIKYKSDGIRGLYOGFSYS 180
DB 121 GAAGATSLCFVYPLDFARTRLADYGVKAGAREPFKGLGDCLVKIKYKSDGIRGLYOGFSYS 180
QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTIIVYSMIAQTVTAAGVSYPFDTVRRMM 240
DB 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTIIVYSMIAQSVTAAGVSYPFDTVRRMM 240
QY 241 OSGRKGADIMYGTVDWCWKIRFDEGKAFKFGAMSNVLRGAGAVLVLYDEIKV 296
DB 241 OSGRKGADIMYGTVDWCWKIRFDEGKAFKFGAMSNVLRGAGAVLVLYDEIKV 296

RESULT 7
ADP1_MOUSE
ID ADP1_MOUSE STANDARD: PRT: 298 AA.
AC P48962; 062164;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (adenine nucleotide translocator 1) (ANT 1) (MANC1).
GN SL25A4 OR AN1 OR ANCL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse homologs.",
RL Mamm. Genome 7:25-30(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/c; TISSUE=Muscle;
RA Laplace C., Costet P.;
RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes.",
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation in the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way


```

Db 121 AAGATSLCFYVPLDFARTRLAADVGKGAQREFGLGNCILTKIFKSGLGLVGFENVSV 160
Oy 182 OGIIITPAATFEGYDTAKGMLPDKPKNTHIVSWMIAOTVAAGVSVPFDFVRRMMQ 2411
Db 181 OGIIITPAATFEGYDTAKGMLPDKPKNTHIVSWMIAOTVAAGVSVPFDFVRRMMQ 2400
Oy 242 SGRKGADIMTWGTGVCADKRIKIFRDEGCKAFPKFGAMSNVLKMGCAFVYLVDLKKVI 298
Db 241 SGRKGADIMTWGTGVCADKRIKIFRDEGCKAFPKFGAMSNVLKMGCAFVYLVDLKKVI 297

RESULT 9
ADT1 HUMAN
ID ADP1 HUMAN STANDARD; PRT; 298 AA.
AC p12235:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE-89236396; PubMed-2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
RT ADP/ATP translocase."
RT J. Mol. Biol. 206:261-280(1989).
RN 12
RP SEQUENCE FROM N.A.
RX MEDLINE-89340499; PubMed-2547778;
RA Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
RA Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
RT "A human muscle adenine nucleotide translocator gene has four exons,
RT 1 is located on chromosome 4, and is differentially expressed."
RT J. Biol. Chem. 264:13998-14004(1989).
RN 13
RP SEQUENCE FROM N.A.
RX MEDLINE-88041149; PubMed-2823266;
RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack
RT of a leader peptide, divergence from a fibroblast translocator cDNA,
RT and coevolution with mitochondrial DNA genes."
RT Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
RN 14
RP SEQUENCE FROM N.A.
RX TISSUE-Eye;
RA Strausberg R.;
RN Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE OF 1-37 FROM N.A.
RX TISSUE-Liver;
RA MEDLINE-88124845; PubMed-2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RT Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
RN 16
RP VARIANTS PEO PRO-114 AND MET-289.
RX MEDLINE-20385067; PubMed-10926541;
RA Kaukonen J., Juselius J.K., Tiranti V., Kyttala A., Zeviani M.,
RA Comi G.P., Keraian J., Pellonen L., Suomalainen A.;
RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance."
RT Science 289:782-785(2000).
RN 17
RP FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.

```

```
CC -I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC CCSE- Detecter In SLC25A4 are a cause of autosomal dominant  
CC progressive external ophthalmoplegia with various mitochondrial  
CC DNA deletions (PEO). Patients with PEO have mtchondrial  
CC atrophy, progressive extermal ophthalmoplegia, and other  
CC abnormalities associated with multiple different deletions of  
CC mitochondrial DNA.  
CC  
CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC The European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isdb.ch/announce/  
CC or send an email to license@isb-sib.ch).  
-----  
DR EMBL; J02966; AAA61223.1; -.  
DR EMBL; J03593; AAA86751.1; -.  
DR EMBL; J04982; AAB51736.1; -.  
DR EMBL; BC008664; AAH08664.1; -.  
DR PIR; A28116; A28116.  
DR PIR; A39891; A39891.  
DR PIR; S03893; S03893.  
DR PIR; A44778; A44778.  
DR Genev; HGNC:10990; SLC25A4.  
DR MIM; 103220; -.  
DR MIM; 157640; -.  
DR InterPro; IPR002067; mlt_carrier.  
DR InterPro; IPR001993; Mitoch_carrler.  
DR Pfam; PF00153; mito_carr; 3.  
DR PRINTS; PR00926; MITOCARRIER.  
DR PROSITE; PS00215; MITOCH_CARRIER; 3.  
KW Mitochondiondri; Inner membrane; Repeat; Transmembrane; Transport;  
KW Multigene family; Disease mutation.  
FT TRANSMEM 12 29 1 (POTENTIAL) .  
FT TRANSMEM 73 91 2 (POTENTIAL) .  
FT TRANSMEM 117 134 3 (POTENTIAL) .  
FT TRANSMEM 176 195 4 (POTENTIAL) .  
FT TRANSMEM 214 231 5 (POTENTIAL) .  
FT TRANSMEM 273 291 6 (POTALIAL) .  
FT REPEAT 1 110 1B .  
FT REPEAT 111 208 2. .  
FT REPEAT 209 298 3. .  
FT VARIANT 114 114 A-> P (IN PEO).  
FT FT VARIANT 289 289 /FTId=VAR_012111.  
FT CONFLICT 16 16 G-> M (IN PEO).  
FT CONFLICT 147 149 KGA-> A (IN REF. 3).  
FT CONFLICT 227 227 V-> L (IN REF. 3).  
SQ SEQUENCE 298 AA; 33064 MW; 59FDDFAEC4E7CFBB CRC64;  
  
Query Match Best Local Similarity 91.3%; Score 1409; DB 1; Length 298;  
Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0.
```

QY 241 OSGRKGADIMYGTGTCMKRIIFNDEGKAFKFGAMSVNLGMGAFVLYLDELKRVY 298
 DB 241 OSGRKGADIMYGTGTCMKRIAKDEGAKAFKFGAMSVNLGMGAFVLYLDELKRVY 298
 RESULT 10
 ADT_DROME STANDARD; PRT; 297 AA.
 AC Q26365; Q26254; P91614; Q9V270;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUN-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP/ATP carrier protein (ADP/ATP translocase) (adenine nucleotide translocator) (ANT) (stress sensitive B protein).
 GN SSB OR A/A-T OR CG16944.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92389367; PubMed=1387687;
 RA Louvi A., Tsiftlidou S.G.;
 RT "A cDNA clone encoding the ADP/ATP translocase of Drosophila melanogaster shows a high degree of similarity with the mammalian ADP/ATP translocases.";
 RL J. Mol. Evol. 35:44-50(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94350065; PubMed=7520869;
 RA Hutter P., Karch F.;
 RT "Molecular analysis of a candidate gene for the reproductive isolation between sibling species of Drosophila.";
 RL Experientia 50:749-762(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R;
 RA Zhang Y.Q., Davis A.W., Roote J., Hermann S., Ashburner M.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Morten J.R., Yandell M.D., Zhang Q., Chen L.X., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasly E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolisakov S., Borokva D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos R., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson R., Dou P.L., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Hostin N., Houston K.A., Howard T.J., Wei M.-H., Ibegwam C., Jajalal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D., Merkllov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M., Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,
 RA Stryker R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER (BT SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (By similarity).
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 DR EMBL; S43651; AAB23114.1; -;
 DR EMBL; S71762; AAB31734.3; -;
 DR EMBL; Y10618; CAA71628.1; -;
 DR EMBL; AEO03484; AAF47957.1; -;
 DR FlyBase; FBgn0003360; sssB.
 DR InterPro; IPR002067; MLC_carrier.
 DR InterPro; IPR001993; MLC_carrier.
 DR Pfam; PF00153; mltc_carri; 3.
 DR PRINTS; PR00926; MITOCH_CARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR MITOCHondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 14 31 1 (POTENTIAL).
 FT TRANSMEM 75 93 2 (POTENTIAL).
 FT TRANSMEM 119 136 3 (POTENTIAL).
 FT TRANSMEM 177 196 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 272 290 6 (POTENTIAL).
 FT CONFLICT 18 19 QV -> GI (IN REF. 3 AND 4).
 FT CONFLICT 81 81 QV -> Y (IN REF. 1).
 FT CONFLICT 200 200 R -> RG (IN REF. 3 AND 4).
 FT CONFLICT 266 266 G -> A (IN REF. 2).
 FT CONFLICT 267 268 PC -> TGA (IN REF. 3 AND 4).
 FT CONFLICT 268 268 C -> S (IN REF. 1).
 SQ SEQUENCE 297 AA; 32880 MW; AA639439968F9750 CRC64;
 Query Match 78.9%; Score 1217.5; DB 1; Length 297;
 Best Local Similarity 79.3%; Pred. No. 4.7e-101;
 Matches 233; Conservative 24; Mismatches 34; Indels 3; Gaps 3;
 QY 5 AISPAPKFLAGGTAIAISKTAIVAPIERVKLLLOVQHASKQIADKQYKGYVDCIAPRKE 64
 DB 7 AVGVGKDFPAAGOVSAASKTAIVAPIERVKLLLOVQHSKQISPKQYKGVWDFIRIPKE 66
 QY 65 QGVTSFWRGNLANVIRFEPQALNFAFKDKYKQIFGQVVKHGFWMYFPFGNLSAGGAAG 124
 DB 67 QGVTSFWRGNLANVIRFEPQALNFAFKDKYKQIFGQVVKHGFWMYFPFGNLSAGGAAG 126
 QY 125 ATSLCFYVPLDFAFTRLAADVKGSTREFRGLDCLVKTTSKSDGIGLYQGSFVSQGI 184
 DB 127 ATSLCFYVPLDFAFTRLAADVKGKQ -QRETFGLGNCGLTKIFKSGDYGVLRGFVSQGI 185
 QY 185 IITYAAVFGYDTAKGLPDKNTHIVSWMIQTVTAAGVSVSPDPYVRRRMMQSGR 244
 DB 186 IITYAAVFGYDTPAR-MLPPKPNPIYISWAIQOVTVTVAGIVSPDPYVRRRMMQSGR 244
 QY 245 KGAIDIMYGTGTCMKRIIFNDEGKAFKFGAMSVNLGMGAFVLYLDELKRVY 298
 DB 245 KATEVITYKNTLHCWATIAKOE-GPCFFKGAFSNLRKGTGAFVLYLDELKRVY 297

Dh	181	VSVGGIIITVRAAYGCGCFDPAKGLMPLDPKNTSLFVSMALAQVYTTAGSGLISVPDFVRRRM	240
Oy	239	MWOSGRKADIMTGYCTUDCMKRIFDEEGCAAFPFKGCAMSNVLRGMGAAFYLVYLDELAKVI	298
Dh	241	WMQSPCKSEVMYKNWTDLDMWKIKQEQSGAEPFKGAFNSNLRTGTGALVLFVEYEVKALL	300
<hr/>			
RESULT 12			
ID	ADLT_CHKKE	STANDARD:	PRT: 339 AA.
AC	P31692;		
DT	01-JUL-1993	(Rel. 26,	Created)
DT	01-JUL-1993	(Rel. 26,	Last sequence update)
DT	15-JUL-1998	(Rel. 36,	Last annotation update)
DE	ADP,ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).		
OC	Chloroxela kessleri.		
OC	Eukaryota; Viridiplantae;		
OC	Chlorophyta; Chlorophyceae;		
OC	NCB1_TaxId=3074;		
RX	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=92084708; PubMed=1748677;		
RA	Hilgarch C., Sauer N., Tanner W.;		
RT	"Glucose increases the expression of the ATP/ADP translocator and the glyceraldehyde-3-phosphate dehydrogenase genes in Chlorella.";		
RL	J Biol. Chem. 265:2404-2404(1991)		
CC	-I- PUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.		
CC	-I- SUBUNIT: HOMODIMER (BY SIMILARITY).		
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.		
CC	-I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.		
CC	-I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.		
CC	this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on ways CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).		
CC	or send an email to license@sib-sib.ch).		
CC	-----		
DR	EMBL; M76669; AAA33027.1; .		
DR	PIR; A41677; A41677.		
DR	InterPro; IPR002067; Mt_carrier.		
DR	InterPro; IPR001993; Mitoch_carrier.		
DR	Pfam; PF00153; mtlo_carr; 3		
DR	PRINTS; PR00926; MITOCARRIER.		
DR	PROSITE; PS00215; MITOCH_CARRIER; 3.		
KW	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.		
FT	TRANSMEM 45 62 1 (POTENTIAL).		
FT	TRANSMEM 108 126 2 (POTENTIAL).		
FT	TRANSMEM 151 168 3 (POTENTIAL).		
FT	TRANSMEM 209 228 4 (POTENTIAL).		
FT	TRANSMEM 248 265 5 (POTENTIAL).		
FT	TRANSMEM 304 322 6 (POTENTIAL).		
SO	SEQUENCE 339 AA; 36686 MW; 54779734A33B3942 CRC64;		
<hr/>			
Query Match 63.4%; Score 978; DB 1; Length 339;			
Best Local Similarity 66.9%; Pred. No. 1.Je-79;			
Matches 198; Conservative 26; Mismatches 64; Indels 8; Gaps 5;			
Oy	6	ISFANDFLAGIAAISKTAVAPIERVKLLLOVGHASKOIADK--QYKGIVDCIVRIPK	63
Dh	39	MAFVDLLAGTAGAISKTAVAPIERVKLLLOVGHASKOIADK--QYKGIVDCIVRIPK	63
Oy	64	EOGVLSFNRGNLANVIRKFFPOALFAFRKDKYKKOLFGLGVGDKNHPFWMYFAGNLAGSGAA	123
Dh	99	EOGVASFPNRGNLANVIRKFFPOALFAFRKDKYKKOLFGLGVGDKNHPFWMYFAGNLAGSGAA	157
Oy	124	GATSLGFVFYPLDFAFTRTLAADVGKSGTEREFGLDGCLVTKITSQDIGLTVOGSFVSVOG	183

```

Db 158 GAGSLIVPLDFARTRLADAVG--SGKSRFETGLVDCISKVRGRGMALYOGFVSGVQG 216
QY 184 IITRYRAAYFQVDTAKGML-PDPKNTIIVYSMMIAQVTVAVGVSPPTVRRMMOS 242
Db 217 IITRYRAAYFQVDTAKGML-PDPKNTIIVYSMMIAQVTVAVGVSPPTVRRMMOS 276
QY 243 GRKADIMYGTVDWCKRIFRDEGKAFFKAGMSNVLRCMGAFVLYLYDELKVI 298
Db 277 ---GGERQVNGTIDCWKRKVAQOGCKMAFFKAGMSNVLRCMGAFVLYLYDELKVI 329

RESULT 13
ADT3_YEAST STANDARD: PRT; 307 AA.
AC P18238:
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 01-OCT-1994 (Rel. 30, Last annotation update)
DE ADP/ATP carrier protein 3 (ADP/ATP translocase 3) (Adenine nucleotide
translocator 3) (ANT 3).
GN AAC3 OR YBR085W OR YBR0753.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90324259; PubMed=2165073;
RA Kolarov J., Kolarova N., Nelson N.;
RT "A third ADP/ATP translocator gene in yeast.";
RL J. Biol. Chem. 265:12711-12716(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RA Andre B., Cziepluch C., Hein C., Jauniaux J.C., Urrestarazu A.,
RA Viessers S.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 38-307 FROM N.A.
RC STRAIN=S288c;
RA Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M34076; AAA97485.1; -
DR EMBL; Z35954; CAAB5031.1; -
DR PIR; A36582; A36582.
DR SGD; S0000289; AAC3.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCH_CARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 16 33 1 (POTENTIAL).
FT TRANSMEM 78 96 2 (POTENTIAL).
FT TRANSMEM 120 137 3 (POTENTIAL).

```

```

FT TRANSMEM 181 200 4 (POTENTIAL).
FT TRANSMEM 220 237 5 (POTENTIAL).
FT TRANSMEM 276 294 6 (POTENTIAL).
SQ SEQUENCE 307 AA; 3313 MW; DDC1329FEC1B4DC8 CRC64;

Query Match 50.5%; Score 778.5; DB 1; Length 307;
Best local Similarity 53.7%; Pred. No. 5,3e-62;
Matches 161; Conservative 45; Mismatches 85; Indels 9; Gaps 5;

QY 3 EQAISFAKDFLAGGIAAISKTAVPATERYKLLQVQ--HASKRLADADKQKGIIVDCIVR 61
Db 7 QOETNFAINFLEMGVSAIAIKTASPTERYKLLQVQDEMIKQGTLDKKSGLVDCPKRT 66
QY 62 PKEGVLSPWRGNLIANYIRFPTQALNFAFKDKYKQIFLGVDKHTQFMYRFAGNLASG 121
Db 67 AKQEGSLSPWRGNLVANIRKFPQALNFAFKDKIKLMF--GFKKEBGGWGFAGNLASG 124
QY 122 AAGATSLCEVYPLDFARTRLADAV--GKSGTEREPNGLDCLVKTSGDGRGLYGFV 179
Db 125 AAGATSLCEVYPLDFARTRLADAV--GKSGTEREPNGLDCLVKTSGDGRGLYGFV 184
QY 180 SVGGIITRYRAAYFQVDTAKGML-LPDPKNTIIVYSMMIAQVTVAVGVSPPTVRRM 238
Db 185 SVGGIITRYRAAYFQVDTAKGML-LPDPKNTIIVYSMMIAQVTVAVGVSPPTVRRM 244
QY 239 MMSGKRGADIMYGTVDWCKRIFRDEGKAFFKAGMSNVLRCMGAFVLYLYDELKVI 298
Db 245 MMSGKRGADIMYGTVDWCKRIFRDEGKAFFKAGMSNVLRCMGAFVLYLYDELKVI 301

RESULT 14
ADT_CHLRE STANDARD: PRT; 308 AA.
AC P27080;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE 01-OCT-1994 (Rel. 30, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
translocator) (ANT).
GN ABT.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadales; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FUD4-R2;
RA MEDLINE=93204887; PubMed=8455552;
RA Sharpe J.A., Day A.;
RT "Structure, evolution and expression of the mitochondrial ADP/ATP
translocator gene from Chlamydomonas reinhardtii.";
RL Mol. Gen. Genet. 237:134-144(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X65194; CAA46311.1; -
DR PIR; S30259; S30259.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.

```


PRINTS: PRO0926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER: 2.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 74 92 2 (POTENTIAL).
 FT TRANSMEM 116 133 3 (POTENTIAL).
 FT TRANSMEM 178 197 4 (POTENTIAL).
 FT TRANSMEM 217 234 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 SQ SEQUENCE 308 AA; 33528 MW; DA77CF0E72B7A53F CRC64;
 Query Match
 Best Local Similarity 51.8%; Score 772; DB 1; Length 308;
 Matches 157; Conservative 55; Mismatches 81; Indels 10; Gaps 5;
 QY 1 MTEQAISEKDFLAGIAAISKTVAPIERVKLLQVO-HASKQIADKQYGVDCIV 59
 DB 1 MAKEENFVAVDLGAGLSAAVSKTAAPRIERYKLLIONODEMIKQRLASPYKGICECV 60
 QY 60 RIPEKQGVLSFWRGNLANVIRFPQALNFARFKDKYKQJELGVDKHHQFMRYEGNLAS 119
 DB 61 RIVREKGGSLRGRNTANVIRFPQALNFARFKDKYKQJELGVDKHHQFMRYEGNLAS 118
 QY 120 GGAAGATSLCFEYVPLDFARTRLAAD--VGKSTEREFRGLDCLVKTSGIRGLYOG 176
 DB 119 GGAAGAVSLSFYSLDYARTRLANDAKSAKGGDRQNGLVYRKRTIASDGIAGLYRG 178
 QY 177 FEVSVOGIIITRAAFGVYDTAKG-MLPDPKNTHTVSMIAQTVTAAGVSPYDITVR 235
 DB 179 FNISCGIVYVGLFVGMDSLKPVVLVGPLANNFLAFLMGITIGGLASYPIDITR 238
 QY 236 RRMHMOGSRGADIMYTGVDCKRIFRDEGKAPFKGAMSVNLRMGAPFLVLTDELK 295
 DB 238 RRMHMTS---GSAVKNSSFRFOELVKNKGKSLFKFGAAILRAVAGVLAGITDQLQ 295
 QY 296 KVI 298
 DB 296 VIL 298
 RESULT 15
 ADT_SCHPO STANDARD; PRT; 322 AA.
 ID ADT_SCHPO 009188;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
 GN ANCI OR SPC530.10C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC NCBI_TaxID=4896;
 RN NCBI
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RX MEDLINE-96257204; PubMed-8675018;
 RA Cousin N., Trezequet V., Saux A.L., Lauguin G.J.M.;
 RT "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation in Saccharomyces cerevisiae."
 RL Gene 171:113-117(1996).
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RX MEDLINE-21848401; PubMed-11859360;
 RA Wood V., Galliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgourou J., Peat N., Hajles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald D., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quill M.A., Rabinovitch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tiley A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkerts G., Aert R., Robben J., Gymnopoulos B.,
 RA Weljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritze C., Holzer C., Reinhardt R., Pohl T.M.,
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Mambutt R., Purrelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S.,
 RA Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
 RA "The genome sequence of Schizosaccharomyces pombe."
 RL Nature 415:871-880(2002).
 CC - FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC - SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC - SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC - DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Z49974; CAA90275.1; -
 DR EMBL: AL023634; CAI9176.1; -
 DR InterPro: IPR002067; MLC_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carrier_3.
 DR PRINTS: PRO0926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER: 2.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 28 48 1 (POTENTIAL).
 FT TRANSMEM 93 111 2 (POTENTIAL).
 FT TRANSMEM 131 151 3 (POTENTIAL).
 FT TRANSMEM 197 217 4 (POTENTIAL).
 FT TRANSMEM 222 242 5 (POTENTIAL).
 FT TRANSMEM 289 309 6 (POTENTIAL).
 SQ SEQUENCE 322 AA; 35020 MW; BAC3D16A4DF41AFC CRC64;
 Query Match
 Best Local Similarity 49.8%; Score 769; DB 1; Length 322;
 Matches 158; Conservative 50; Mismatches 75; Indels 12; Gaps 6;
 QY 7 SFKDFLAGIAAISKTVAPIERVKLLQVOHASKQIADK--QYGVDCIVRIK 63
 DB 26 TFEFDPMGCVSAAVSKTAAPRIERYKLLIONO--DEMIKQRLASPYKGICECVRTAA 83
 QY 64 EGVLSFWRGNLANVIRFPQALNFARFKDKYKQJELGVDKHHQFMRYEGNLASGAA 123
 DB 84 EGVLSLWRGNLANVIRFPQALNFARFKDKYKQJELGVDKHHQFMRYEGNLASGAA 142
 QY 124 GATSLCFEYVPLDFARTRLADV--GKSTEREFRGLDCLVKTSGIRGLYOGFSV 181
 DB 143 GAASLSFVSLDYARTRLANDAKSAKGGDRQNGLVYRKRTIASDGIAGLYRGSP 202
 QY 182 OGIIITRAAFGVYDTAKG-MLPDPKNTHTVSMIAQTVTAAGVSPYDITVR 240
 DB 203 VGIVYVGLFVGMDSLKPVVLVGPLANNFLAFLMGITIGGLASYPIDITR 262

Wed Nov 13 10:40:44 2002

us-09-393-441-33.rsp

Page 12

OY 241 QSGRKADIMYTGTVDCKRIFRDEGGCAFFKGAANSVLRGKGCAFVLVLYDELK 295
 || : | : : | : | | : : ||| : : || : | : :
 Db 263 TSGEA--VKYSSEFECCGRQLIAKEGARSSFFKAGACNILRGVAGAGVLSIYDQVQ 314

Search completed: November 12, 2002, 16:46:28
Job time : 8.67525 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2002, 16:43:45 ; Search time 25.3617 Seconds
(without alignments)
2421.054 Million cell updates/sec

Title: US-09-393-441-33

Perfect score: 1543
Sequence: 1 MFEQAISFAKDFLAGGIAA.....LRGMGAFVLYVLDLKKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SP archaea:*
- 2: SP bacteria:*
- 3: SP fungi:*
- 4: SP human:*
- 5: SP invertebrate:*
- 6: SP mammal:*
- 7: SP mhc:*
- 8: SP organelle:*
- 9: SP phage:*
- 10: SP plant:*
- 11: SP rodent:*
- 12: SP virus:*
- 13: SP vertebrate:*
- 14: SP unclassified:*
- 15: SP virus:*
- 16: SP bacteriophage:*
- 17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1451	94.0	298	6	08SQH5
2	1422	92.2	298	6	046373
3	1421	92.1	298	11	0919M9
4	1418	91.9	298	11	062164
5	1409	91.3	298	13	09PRH1
6	1406	90.9	298	13	09PRH2
7	1402	90.9	298	13	09YIC4
8	1300	84.3	299	5	095VX4
9	1259	81.6	317	13	091336
10	1254.5	80.3	299	5	095S30
11	1235.5	81.1	300	5	09NHWS
12	1187.5	77.0	288	5	044093
13	1183.5	76.7	288	5	044094
14	1176.5	76.2	304	5	025129
15	1137.5	73.7	307	5	062526
16	1119	72.5	315	4	09HOC2

17	1041	67.5	313	5	021103	021103 caenorhabd1
18	1039	67.3	313	5	P91410	P91410 caenorhabd1
19	1038	67.3	300	5	045865	045865 caenorhabd1
20	996	64.5	309	5	097470	097470 dictyostel1
21	993.5	64.4	300	5	001813	001813 caenorhabd1
22	993	64.4	300	5	017407	017407 caenorhabd1
23	973.5	63.1	307	5	09BJ36	09BJ36 toxoplasma
24	946.5	61.3	307	8	09XM22	09XM22 ascaris suu
25	944	61.2	301	5	025692	025692 plasmodium
26	943	61.1	301	5	026006	026006 plasmodium
27	827	53.6	170	6	09X569	09X569 sus scrofa
28	778.5	50.5	305	3	09P8M1	09P8M1 yarrowia 11
29	764	49.5	326	5	P91270	P91270 caenorhabd1
30	760	49.3	307	5	076286	076286 trypanosoma
31	759	49.2	303	3	074260	074260 candida par
32	756.5	49.0	306	5	018683	018683 caenorhabd1
33	753	48.8	307	5	026697	026697 trypanosoma
34	747	48.4	306	3	P78754	P78754 schistosacch
35	744	48.2	388	10	049875	049875 lupinus alb
36	743	48.2	379	10	049447	049447 arabidopsis
37	743	48.2	386	10	P93767	P93767 lycopersico
38	734	47.6	331	10	041628	041628 triticum tu
39	731.5	47.4	305	3	09P876	09P876 pichia jadt
40	731	47.4	317	5	09N647	09N647 leishmania
41	728.5	47.2	305	3	09P875	09P875 pichia jadt
42	724.5	47.0	308	3	08TEK7	08TEK7 neocallim
43	688.5	44.6	330	10	09FEM8	09FEM8 arabidopsis
44	681.5	44.2	298	5	021809	021809 caenorhabd1
45	653.5	42.4	262	10	09AVT6	09AVT6 picea abies

ALIGNMENTS

RESULT 1
08SQH5 PRELIMINARY; PRT; 298 AA.
AC 08SQH5;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adenine nucleotide translocator 2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN 11
RP SEQUENCE FROM N.A.
RA Yamazaki N., Shinohara Y., Tanida K., Terada H.;
RT "Structural properties of mammalian mitochondrial ADP/ATP carriers:
RT Identification of possible amino acids that determine functional
RT differences in its isoforms.";
RL Mitochondrion 1:371-379(2002).
DR EMBL: AB065433; BAB84673.1;
SQ SEQUENCE 298 AA; 3295 MM; CB6897BB987B79C0 CRC64;

Query Match 94.0%; Score 1451; DB 6; Length 298;
Best Local Similarity 92.2%; Pred. No. 5e-119;
Matches 273; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY	1	MFEQAISFAKDFLAGGIAAISKTRAVAPIERVKLLLOVQHSKQIADKQKGIYDCIVR	60
DB	1	MTDAVSFAKDFLAGGVAALSKTRAVAPIERVKLLLOVQHSKQITADKQKGIIDCVVR	60
QY	61	IPKCGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHKQFMFYPAGNLASG	120
DB	61	IPKCGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHKQFMFYPAGNLASG	120
QY	121	GAAGTSLCEFYPLDFAFTRILADVGSKTEREFRGLDCLVTKTSDGIRGLYOGFSVS	180
DB	121	GAAGTSLCEFYPLDFAFTRILADVGSKTEREFRGLDCLVTKTSDGIRGLYOGFSVS	180

QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTHTLVSMIAQTAVAGVSYSPDVTYRRMM 240
 DB 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTHTLVSMIAQTAVAGVSYSPDVTYRRMM 240
 QY 241 QSGRKGADIMYGTVDCKRIKADDEGAKAFKFGAMSNVLRGMGAFVLYDELKK 296
 DB 241 QSGRKGADIMYGTVDCKRIKADDEGAKAFKFGAMSNVLRGMGAFVLYDELKK 296

RESULT 2

046373 PRELIMINARY: PRT: 298 AA.
 AC 046373;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE ADP/ATP translocase.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NC NCBL_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SKELETAL MUSCLE;
 RA Yamauchi N., Kasai M.;
 RT Identification of a 30kDa calsequestrin-binding protein, which
 RT regulates calcium release from sarcoplasmic reticulum of rabbit
 RT skeletal muscle.".
 RL J. Biochem. 335:541-547(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB009386; BAA23777.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carrier_3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCARRIER.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA: 32901 MW: 3288164AD78 CRC64;

Query Match 92.2%; Score 1422; DB 6; Length 298;
 Best local similarity 88.9%; Pred. No. 1,7e-116;
 Matches 265; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQAIISFAKDFLAGGIAAISTAVAPIERVKLLQVOHASKQIADRYKQKIVDCYR 60
 DB 1 MTEQAIISFAKDFLAGGIAAISTAVAPIERVKLLQVOHASKQIADRYKQKIVDCYR 60
 QY 61 IPKEGVLSEFMGNLANVIRYPTQALNFAFKKRYKQIFLGVDKTOFWRRYFAGNLAG 120
 DB 61 IPKEGVLSEFMGNLANVIRYPTQALNFAFKKRYKQIFLGVDKTOFWRRYFAGNLAG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGIDGCLVITKTSRIGLYOGFSVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGIDGCLVITKTSRIGLYOGFSVS 180
 QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTHTLVSMIAQTAVAGVSYSPDVTYRRMM 240
 DB 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTHTLVSMIAQTAVAGVSYSPDVTYRRMM 240
 QY 241 QSGRKGADIMYGTVDCKRIKADDEGAKAFKFGAMSNVLRGMGAFVLYDELKKVI 298
 DB 241 QSGRKGADIMYGTVDCKRIKADDEGAKAFKFGAMSNVLRGMGAFVLYDELKKVI 298

RESULT 3

0919M9 PRELIMINARY: PRT: 298 AA.
 AC 0919M9;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Adenine nucleotide translocase.
 GN ANTI.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 NC NCBL_TaxID=8335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Crawford M.J., Khosrowshahian F., Yarmuza S.L., Liversage R.A.;
 RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
 RT Dynamic Patterns of Expression During Development."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF231347; AAF63471.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carrier_3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCARRIER.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA: 32940 MW: 91874013751877F CRC64;

Query Match 92.1%; Score 1421; DB 13; Length 298;
 Best local similarity 90.3%; Pred. No. 2,1e-116;
 Matches 269; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQAIISFAKDFLAGGIAAISTAVAPIERVKLLQVOHASKQIADRYKQKIVDCYR 60
 DB 1 MTEQAIISFAKDFLAGGIAAISTAVAPIERVKLLQVOHASKQIADRYKQKIVDCYR 60
 QY 61 IPKEGVLSEFMGNLANVIRYPTQALNFAFKKRYKQIFLGVDKTOFWRRYFAGNLAG 120
 DB 61 IPKEGVLSEFMGNLANVIRYPTQALNFAFKKRYKQIFLGVDKTOFWRRYFAGNLAG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGIDGCLVITKTSRIGLYOGFSVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGIDGCLVITKTSRIGLYOGFSVS 180
 QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTHTLVSMIAQTAVAGVSYSPDVTYRRMM 240
 DB 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTHTLVSMIAQTAVAGVSYSPDVTYRRMM 240
 QY 241 QSGRKGADIMYGTVDCKRIKADDEGAKAFKFGAMSNVLRGMGAFVLYDELKKVI 298
 DB 241 QSGRKGADIMYGTVDCKRIKADDEGAKAFKFGAMSNVLRGMGAFVLYDELKKVI 298

RESULT 4

062164 PRELIMINARY: PRT: 298 AA.
 AC 062164;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Adenine nucleotide carrier (Adenine nucleotide translocase 1) (Similar
 DE to solute carrier family 25 (Mitochondrial carrier, adenine nucleotide
 DE translocator), member 4) (Hypothetical 32.9 kDa protein).
 GN SLC25A4 OR MNC1 OR ANTI.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBL_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE=MUSCLE;
 RA Laplace C., Costet P.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.:
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 translocase 1 and 2 genes."
 RN Submitted (Mar-2000) to the EMBL/Genbank/DBJ databases.
 RL [3]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.:
 RL Submitted (Feb-2001) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Tissue-Eye.
 RC Strausberg R.:
 RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: X74510; CA52616.1; -.
 DR EMBL: AF240002; AAF64470.1; -.
 DR EMBL: BC026925; AAH03791.1; -.
 DR EMBL: BC026925; AAH03791.1; -.
 DR MGI: 1353495; Slc25a4.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Hypothetical protein; Inner membrane; Repeat; Transmembrane;
 KW Transport; Mitochondrion.
 SQ SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CRC64;

Query Match 91.9%; Score 1418; DB 11; Length 298;
 Best Local Similarity 88.9%; Pred. No. 3.9e-116;
 Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

OY 1 MTEQATSFADKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQYGIYV 60
 DB 1 MDDQALSFADKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQYGIYV 60
 OY 61 IREQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKTKQTFWRPAGMLASG 120
 DB 61 IREQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKTKQTFWRPAGMLASG 120
 OY 61 IREQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKTKQTFWRPAGMLASG 120
 DB 61 IREQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKTKQTFWRPAGMLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGDGLCTKIFKSDGLKGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGDGLCTKIFKSDGLKGLYQGFVS 180
 OY 181 VGGIIRAAVFGVYDTAKGMLPDPKNTHTIVSMIAQTAVAGVSYPFDTVRRRMM 240
 DB 181 VGGIIRAAVFGVYDTAKGMLPDPKNTHTIVSMIAQTAVAGVSYPFDTVRRRMM 240
 OY 241 OSGRKADIMYGTGVDCKRKIFDEGKAFKFGAMSNTLGMGAFVLVLYDELKRYI 298
 DB 241 OSGRKADIMYGTGVDCKRKIFDEGKAFKFGAMSNTLGMGAFVLVLYDEIKRYV 298

RESULT 5

O9PRH1 PRELIMINARY; PRT; 298 AA.
 AC O9PRH1:
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana rugosa (Wrinkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9083429; PubMed=9866197;
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.:
 DR "The origin and differentiation of the heteromorphic sex chromosomes

RT Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
 RT a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB008463; BAA36513.1; -.
 DR EMBL: AB008456; BAA36506.1; -.
 DR EMBL: AB008461; BAA36511.1; -.
 DR EMBL: AB008462; BAA36512.1; -.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR002030; Mlt_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56548D36 CRC64;

Query Match 91.3%; Score 1409; DB 13; Length 298;
 Best Local Similarity 88.6%; Pred. No. 2.4e-115;
 Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

OY 1 MTEQATSFADKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQYGIYV 60
 DB 1 MDDQALSFADKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQYGIYV 60
 OY 61 IREQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKTKQTFWRPAGMLASG 120
 DB 61 IREQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKTKQTFWRPAGMLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGDGLCTKIFKSDGLKGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGKSGTEREFGDGLCTKIFKSDGLKGLYQGFVS 180
 OY 181 VGGIIRAAVFGVYDTAKGMLPDPKNTHTIVSMIAQTAVAGVSYPFDTVRRRMM 240
 DB 181 VGGIIRAAVFGVYDTAKGMLPDPKNTHTIVSMIAQTAVAGVSYPFDTVRRRMM 240
 OY 241 OSGRKADIMYGTGVDCKRKIFDEGKAFKFGAMSNTLGMGAFVLVLYDELKRYI 298
 DB 241 OSGRKADIMYGTGVDCKRKIFDEGKAFKFGAMSNTLGMGAFVLVLYDEIKRYI 298

RESULT 6

O9PRH2 PRELIMINARY; PRT; 298 AA.
 AC O9PRH2:
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana rugosa (Wrinkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9083429; PubMed=9866197;
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.:
 RT "The origin and differentiation of the heteromorphic sex chromosomes
 Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
 a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB008460; BAA36510.1; -.
 DR EMBL: AB008458; BAA36508.1; -.
 DR EMBL: AB008459; BAA36509.1; -.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.

DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr. 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MITOCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER. 3.
 KW Inner membrane: Mitochondrion; Transmembrane: Transport.
 SQ SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;

Query Match 91.1%; Score 1406; DB 13; Length 298;
 Best Local Similarity 88.3%; Pred. No. 4,4e-115;
 Matches 263; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQATSFADFLAGGAAIAISKTAAPIERVKLLQVHASKQIADKQYKGTVDICVR 60
 DB 1 MTAATISFADFLAGVAAAISKTAAPIERVKLLQVHASKQIADKQYKGTVDICVR 60
 QY 61 IPKEQGLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
 DB 61 IPKEQGLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
 QY 121 GAAGATSLCEVYPLDFARTRLADVGKSGTEREFGIGDCLVTKSDGIRGLYQGFVS 180
 DB 121 GAAGATSLCEVYPLDFARTRLADVGKAGADREFKGLGDCIAKIFRSDGILKGLYQGFVS 180
 QY 181 VQGIITIRAAVFGYVDPAKGMPLDPKNTHTIVSMIAQVTAAGVSYSPDYRRRMM 240
 DB 181 VQGIITIRAAVFGYVDPAKGMPLDPKNTHTIVSMIAQVTAAGVSYSPDYRRRMM 240
 QY 241 QSGRKGADIMVTGTVDCWKRIFRDEGGAFFKAGMSNVLRGMGAFLVLYDELKVI 298
 DB 241 QSGRKGAEIMVSGTIDCWKKIARDEGSRAPFKAGMSNVLRGMGAFLVLYDELKVI 298

RESULT 7
 QYIC4 PRELIMINARY; PRT; 298 AA.

ID 09YIC4
 AC 09YIC4:
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana rugosa (Trinked frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 OX NCBI_TaxID=6410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99083429; Pubmed=9866197;
 RA Mura I., Ohnishi H., Nakamura M., Ichikawa Y., Saitoh K.;
 RT "The origin and differentiation of the heteromeric sex chromosomes
 Z, W, X, and Y in the frog Rana rugosa. Inferred from the sequences of
 a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619 (1998).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY)
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB008457; BA36507.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr. 3
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MITOCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER. 3.
 KW Inner membrane: Mitochondrion; Transmembrane: Transport.
 SQ SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match 90.9%; Score 1402; DB 13; Length 298;
 Best Local Similarity 87.9%; Pred. No. 9,8e-115;
 Matches 262; Conservative 21; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MTEQATSFADFLAGGAAIAISKTAAPIERVKLLQVHASKQIADKQYKGTVDICVR 60
 DB 1 MTAATISFADFLAGVAAAISKTAAPIERVKLLQVHASKQIADKQYKGTVDICVR 60

DB 1 MTDATISFADFLAGVAAAISKTAAPIERVKLLQVHASKQIADKQYKGTVDICVR 60
 QY 61 IPKEQGLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
 DB 61 IPKEQGLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
 QY 121 GAAGATSLCEVYPLDFARTRLADVGKSGTEREFGIGDCLVTKSDGIRGLYQGFVS 180
 DB 121 GAAGATSLCEVYPLDFARTRLADVGKAGADREFKGLGDCIAKIFRSDGILKGLYQGFVS 180
 QY 181 VQGIITIRAAVFGYVDPAKGMPLDPKNTHTIVSMIAQVTAAGVSYSPDYRRRMM 240
 DB 181 VQGIITIRAAVFGYVDPAKGMPLDPKNTHTIVSMIAQVTAAGVSYSPDYRRRMM 240
 QY 241 QSGRKGADIMVTGTVDCWKRIFRDEGGAFFKAGMSNVLRGMGAFLVLYDELKVI 298
 DB 241 QSGRKGAEIMVSGTIDCWKKIARDEGSRAPFKAGMSNVLRGMGAFLVLYDELKVI 298

RESULT 8

ID 095VX4 PRELIMINARY; PRT; 299 AA.
 AC 095VX4:
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ADP-ATP translocator.
 OS Ethmostigmus rubripes.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Myriapoda; Chilopoda;
 OC Pleurostigmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
 OX NCBI_TaxID=62613;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Burnell J.N.;
 RT "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus
 rubripes.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF401758; AL02100.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr. 3.
 DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN. 2.
 SQ SEQUENCE 299 AA; 33037 MW; 3C3BBCB26E7C3C5E CRC64;

Query Match 84.3%; Score 1300; DB 5; Length 299;
 Best Local Similarity 81.5%; Pred. No. 8,5e-106;
 Matches 243; Conservative 26; Mismatches 29; Indels 0; Gaps 0;

QY 1 MTEQATSFADFLAGGAAIAISKTAAPIERVKLLQVHASKQIADKQYKGTVDICVR 60
 DB 1 MPIDAVSFLDFLAGVAAAISKTSVAPIERVKLLQVHASKQIADKQYKGTVDICVR 60
 QY 61 IPKEQGLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
 DB 61 IPQGLSLFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120
 QY 121 GAAGATSLCEVYPLDFARTRLADVGKSGTEREFGIGDCLVTKSDGIRGLYQGFVS 180
 DB 121 GAAGATSLCEVYPLDFARTRLADVGKLEQREFTGNGICIAKIFKSDGLVGLYQGFVS 180
 QY 181 VQGIITIRAAVFGYVDPAKGMPLDPKNTHTIVSMIAQVTAAGVSYSPDYRRRMM 240
 DB 181 VQGIITIRAAVFGYVDPAKGMPLDPKNTHTIVSMIAQVTAAGVSYSPDYRRRMM 240
 QY 241 QSGRKGADIMVTGTVDCWKRIFRDEGGAFFKAGMSNVLRGMGAFLVLYDELKVI 298
 DB 241 QSGRKGADIMVTGTVDCWKRIFRDEGGAFFKAGMSNVLRGMGAFLVLYDELKVI 298

RESULT 9
 ID 091336 PRELIMINARY; PRT; 317 AA.
 AC 091336:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)

Query Match	Similarity	81.6%	Score 1259;	DB 13;	Length 317;
Best Local	Similarity	86.8%	Pred. No. 3.6e-102;		
Matches 236;	Conservative	19;	Mismatches 17;	Indels	0; Gaps
					0;
OY	1 MTEQASIFAKDFLAGGIAAIAIKTAVAPIERKLLQVOHASKQIAADKQYKGIYDCIVR	60			
Db	1 MTDANSTRKADPLAGGVAIAIKTAVAPIERKLLQVOHASKQIATADKQYKGIYDCIVR	60			
OY	61 IPKEQGVLSFWRGNLNANVIRFFPTQALNFAEKOKYKQIFLGGVDXKHTQFMRYFAGNLASG	120			
Db	61 IPKEQGFISFWRGNLNANVIRFFPTQALNFGFKDKYKKEFLDNDVKRTQFMRYFAGNLASG	120			
OY	121 GAAGATSLCFVYPLDPAFRTRLAADYCKSGTSEREFGLDGLCYIKTKSGIIBGLYOGFSYS	180			
Db	121 GAAGATSLCFVYPLDPAFRTRLAADYCKGAGREFNGLDGLCYIKTKSGIIBGLYOGFSYS	180			
OY	181 VGGIITVRAAYEGVDFAKGMLPDKRNTHIVVSMIAQCTVAVAGVSYEPFTVRRMM	240			
Db	181 VGGIITVRAAYEGVIDTAKGMLPDKRNTHIVVSMIAQSVTAVAGFSGIPEFTVRRMM	240			
OY	241 OSGRKGADIMVTGVYDCWKRKIFRDEGKAFFK	272			
Db	241 OSGRKGAELIMVSGTIDCWKKIARDEGGAFFR	272			
RESULT 10					
ID	095S30	PRELIMINARY;	PRT;	299	AA.
AC	095S30;				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)				
DE	GM12886P (LP02726P).				
GN	SESB OR CG16944.				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydroidea; Drosophilidae; Drosophila.				
OX	NCBI_TaxID=7227;				
RN	[1]				
RP	SEQUENCE FROM N.A.				

	Query Match	81.3%	Score 1254.5:	DB 5:	Length 299;
	Best Local Similarity	80.6%;	Pred. No. 8.2e-107;		
	Matches 237; Conservative	23;	Mismatches 33;	Indels 1;	Gaps 1:
Oy	5 AISAFAKDFLAGGIAAISKATAVAPIERYKKLLQVOHASKOJMAADKOYKGIVDCIVRIKPE 64				
Dd	7 AVGFKADEAFAGGISAAISAKSTAVAPIERVKLLQVOHIKSQISPDROKYGMWDCFRIKPE 66				
Oy	65 OGVLSPFWGNLANLVRYEPTOLNFAFDKYQIQLFGVDKHTOWRRPAGNLASGGAAK 124				
Dd	67 OGSFSSFWRONLNAVLRFTPTQALNAFERDKTKQVFLGVGDKNTOQRWRFAGNLASGGAAK 126				
Oy	125 ATSLCFVVPPLDFAARRLAADYKSGCTSEREFRLGLDCLVTKITKSDSIRCLYOGFSYVGII 184				
Dd	127 ATSLCFVVPPLDFAARRLAADTGKGG-QREFTGLGNCILRKIFKSDGIIGVLRGFGVSYVGI 185				
Oy	185 IYYRAAYGCVYTATAGMLPDPKNTIHIVSMIAQVTYAVAGVSPEDOTVRBRMMOSGR 244				
Dd	186 IYYRAAYGCVYDTAGMLPDPKNTPIYISMAIAQVYTVAGVSYPFPTVRBRMMOSGR 245				
Oy	245 KCAIDMYGTGVCWCKRIFRDECGKAFPKGAMSNVLRGMGAFVLVLYDELKKVI 298				
Dd	246 KTEVYIKNTLHGAKNTIAKOEQTGAFFPGCAFESNIILRGTAQVTLVLYDEIKKVL 299				
	RESULT 11				
ID	Q9NHM5	PRELIMINARY;	PRT;	300 AA.	
AC	Q9NHM5;				
DT	01-OCT-2000 (TREMblrel. 15, Created)				
DT	01-OCT-2000 (TREMblrel. 15, Last sequence update)				
DT	01-MAR-2002 (TREMblrel. 20, Last annotation update)				
DE	ADP/ATP translocase.				
OS	Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
CC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OX	Oestroidea; Calliphoridae; Luciflia.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
KC	STRAIN=SS MAL SEEKING;				
RA	Chen Z., Fair J.A., Batterham P.;				
RT	"A cDNA clone encoding the ADP/ATP translocase of luciflia cuprina.";				
RL	Submitted (DEC-1999) to the EMBL/Genbank/DDJ databases.				
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL				
CC	INNER MEMBRANE (BY SIMILARTY).				
CC	- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.				
DR	EMBL: AF218587; AAF32322.1; -				
DR	InterPro: IPRO01993; Mitoch-carrier.				

DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 300 AA; 33036 MW; 5459DFDA0E2E742 CRC64;

Query Match 80.1%; Score 1235.5; DB 5; Length 300;
 Best Local Similarity 79.5%; Pred. No. 3.8e-100;
 Matches 233; Conservative 24; Mismatches 35; Indels 1; Gaps 1;

QY 6 ISPAKDFLAGGIAAISTKTAVERKLLQVOHASKQIADKQYGYDCIARIKEQ 65
 DB 9 LGFVKDFPAAGGISAASKTAVAPRIERVKLLQVOHISKQISPKQYKGMIDCEVRIPEQ 68
 QY 66 GVLSEFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDVHTQFWRYFAGNLASGAAGA 125
 DB 69 GFASVWGNMANNVIRYPTQALNFAFKDKYKQYFGLGVDKNTQFWRYFAGNLASGAAGA 128
 QY 126 TSLCFYVPLDFAFTRRLAADVGSGTEREFGDCLVTKTSKGIRGLYOGFSVSGIIT 185
 DB 129 TSLCFYVPLDFAFTRRLAADVGSGG-OREFTGLGNCLTKIFKSDGLVGLYRGFVSGIIT 187
 QY 186 IYRAAFEGYVDPAKGMIDPKKNTHTVSMIAQVTVAAGVSYPEPTVRRMMQSGRK 245
 DB 188 IYRAAFEGYVDPAKGMIDPKKNTHTVSMIAQVTVAGIVSYPEPTVRRMMQSGRK 247
 QY 246 GADIMYTGVDCKRKIFRDEGKAFKFGKAWSNVLKGMGAFVLYDELKVI 298
 DB 248 ATEIITIKNTIHCWATIAKQEGTGAFFKAGFNSVNLRTGTGAFVLYDELKVI 300

RESULT 12
 ID 044093 PRELIMINARY; PRT; 288 AA.

AC 044093;
 DT 01-JUN-1998 (TEMBLrel. 06, Created)
 DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
 DE 01-MAR-2002 (TEMBLrel. 20, last annotation update)
 DE ADP/ATP translocase (Fragment).
 GN SESB.
 OS Drosophila pseudobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7237;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zeng L.-W., Comeran J.M., Chen B., Kreitman M.;
 RL Genetica 0:0-0(1997).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF025798; AAB87883.1; -.
 DR FlyBase: FBgn0023292; Dpseb; sesb.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 FT NON_TER 288
 FT SEQUENCE 288 AA; 31725 MW; 052B0CC0050436B0 CRC64;

Query Match 77.0%; Score 1187.5; DB 5; Length 288;
 Best Local Similarity 80.7%; Pred. No. 5.8e-96;
 Matches 230; Conservative 19; Mismatches 33; Indels 3; Gaps 3;

QY 5 AIFSAKDFLAGGIAAISTKTAVERKLLQVOHASKQIADKQYGYDCIARIPE 64
 DB 7 AIFGVDFPAAGGISAASKTAVAPRIERVKLLQVOHISKQISPKQYKGMIDCEVRIPE 66
 QY 65 QGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDVHTQFWRYFAGNLASGAAG 124

DB 67 QGFSSFWKGNLANVIRYPTQALNFAFKDKYKQYFGLGVDKNTQFWRYFAGNLASGAAG 126
 QY 125 ATSLCFYVPLDFAFTRRLAADVGSGTEREFGDCLVTKTSKGIRGLYOGFSVSGIIT 184
 DB 127 ATSLCFYVPLDFAFTRRLAADVGSGG-OREFTGLGNCLTKIFKSDGLVGLYRGFVSGIIT 185
 QY 185 IYRAAFEGYVDPAKGMIDPKKNTHTVSMIAQVTVAAGVSYPEPTVRRMMQSGRK 244
 DB 186 IYRAAFEGYVDPAKGMIDPKKNTHTVSMIAQVTVAGIVSYPEPTVRRMMQSGRK 244
 QY 245 KGADIMYTGVDCKRKIFRDEGKAFKFGKAWSNVLKGMGAFVLY 289
 DB 245 KATEIITIKNTIHCWATIAKQEGTGAFFKAGFNSVNLRTGTGAFVLY 288

RESULT 13

ID 044094 PRELIMINARY; PRT; 288 AA.

AC 044094;
 DT 01-JUN-1998 (TEMBLrel. 06, Created)
 DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
 DE 01-MAR-2002 (TEMBLrel. 20, last annotation update)
 DE ADP/ATP translocase (Fragment).
 GN SESB.
 OS Drosophila subobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7241;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zeng L.-W., Comeran J.M., Chen B., Kreitman M.;
 RL Genetica 0:0-0(1997).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF025799; AAB87884.1; -.
 DR FlyBase: FBgn0023237; Dsub; sesb.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR PRINTS: PR00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 FT NON_TER 288
 FT SEQUENCE 288 AA; 31775 MW; 06A1DIE477E81B26 CRC64;

Query Match 76.7%; Score 1183.5; DB 5; Length 288;
 Best Local Similarity 80.4%; Pred. No. 1.3e-95;
 Matches 229; Conservative 20; Mismatches 33; Indels 3; Gaps 3;

QY 5 AIFSAKDFLAGGIAAISTKTAVERKLLQVOHASKQIADKQYGYDCIARIPE 64
 DB 7 AMGVKDFPAAGGISAASKTAVAPRIERVKLLQVOHISKQISPKQYKGMIDCEVRIPE 66
 QY 65 QGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDVHTQFWRYFAGNLASGAAG 124
 DB 67 QGFSSFWKGNLANVIRYPTQALNFAFKDKYKQYFGLGVDKNTQFWRYFAGNLASGAAG 126
 QY 125 ATSLCFYVPLDFAFTRRLAADVGSGTEREFGDCLVTKTSKGIRGLYOGFSVSGIIT 184
 DB 127 ATSLCFYVPLDFAFTRRLAADVGSGG-OREFTGLGNCLTKIFKSDGLVGLYRGFVSGIIT 185
 QY 185 IYRAAFEGYVDPAKGMIDPKKNTHTVSMIAQVTVAAGVSYPEPTVRRMMQSGRK 244
 DB 186 IYRAAFEGYVDPAKGMIDPKKNTHTVSMIAQVTVAGIVSYPEPTVRRMMQSGRK 244
 QY 245 KGADIMYTGVDCKRKIFRDEGKAFKFGKAWSNVLKGMGAFVLY 289
 DB 245 KATEIITIKNTIHCWATIAKQEGTGAFFKAGFNSVNLRTGTGAFVLY 288

[illegible]

